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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:07:03 ; Search time 139.455 Seconds
(without alignments)
981.776 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNYQKSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876	100.0	354	AAE27926	Aae27926 Human CH2
2	1876	100.0	354	ABB82835	Abb82835 Antibody
3	1683	89.7	360	AAE27924	Aae27924 Human CH2
4	1683	89.7	360	ABB82833	Abb82833 Antibody
5	1614	86.0	470	AAE27923	Aae27923 Human C2B
6	1614	86.0	470	ABB82832	Abb82832 Antibody
7	1613.5	86.0	731	AAW52156	Aam52156 Humanised
8	1613.5	86.0	741	AAW52159	Aam52159 Humanised
9	1613	86.0	470	AAW52158	Aam52158 Humanised
10	1608.5	85.7	729	AAW52161	Aam52161 Humanised
11	1608.5	85.7	739	AAW83036	Aaw83036 Anti-Fas
12	1603	85.4	470	AAW814776	Aab14776 Humanised
13	1603	85.4	470	AAW90926	Aaw90926 Humanised
14	1603	85.4	470	ABB74941	Abb74941 Humanised
15	1603	85.4	470	ABB74895	Abb74895 Humanised
16	1603	85.4	470	AD664199	Ad664199 LL2HCF pr
17	1602.5	85.4	465	AAW52157	Aam52157 Humanised
18	1602.5	85.4	730	AAW52160	Aam52160 Humanised
19	1602.5	85.4	740	AAW52161	Aam52161 Humanised
20	1595	85.0	470	AAW90933	Aaw90933 Humanised
21	1595	85.0	470	ABB74902	Abb74902 Humanised
22	1593	84.9	470	AAW90934	Aaw90934 Humanised
23	1593	84.9	470	ABB74903	Abb74903 Mouse hum
24	1592	84.9	470	AAW83037	Aaw83037 Anti-Fas
25	1592	84.9	470	AAW814779	Aab14779 Humanised

26	1592	84.9	470	3	AAW90935	Aaw90935 Humanised
27	1592	84.9	470	3	AAW90929	Aaw90929 Humanised
28	1592	84.9	470	5	ABB74944	Abb74944 Humanised
29	1592	84.9	470	5	ABB74898	Abb74898 Humanised
30	1592	84.9	470	5	ABB74904	Abb74904 Mouse hum
31	1579	84.2	470	3	AAW90936	Aaw90936 Humanised
32	1579	84.2	470	5	ABB74945	Abb74945 Humanised
33	1577.5	84.1	465	4	AAW72228	Aab72228 Humanised
34	1573.5	83.9	464	8	ADJ11354	Adj11354 BHA10 V1#
35	1572.5	83.8	464	4	AAW72232	Aab72232 Humanised
36	1565.5	83.4	467	6	ADA47341	Ada47341 TRX1 agly
37	1565.5	83.4	467	6	ADA47334	Ada47334 TRX1 heav
38	1565.5	83.4	467	6	ADA47336	Ada47336 TRX1 heav
39	1565.5	83.4	467	6	ADA47342	Ada47342 TRX1 agly
40	1565.5	83.4	467	8	ADP88454	Adp88454 Antibody
41	1565.5	83.4	467	8	ADP88446	Adp88446 Antibody
42	1565.5	83.4	467	8	ADP88430	Adp88430 Antibody
43	1565.5	83.4	467	8	ADP88438	Adp88438 Antibody
44	1565.5	83.4	467	8	ADQ87966	Adq87966 Heavy cha
45	1565.5	83.4	467	8	ADQ87970	Adq87970 Heavy cha

ALIGNMENTS

RESULT 1
AAE27926
ID AAE27926 standard; protein; 354 AA.
XX AC AAE27926;
XX AC AAE27926;
DT 27-DEC-2002 (first entry)
XX Human CH2 domain deleted CC49 antibody heavy chain protein.
KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX Homo sapiens.
OS WO200260955-A2.
PN 08-AUG-2002.
PD 29-JAN-2002; 2002WO-US002373.
XX 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
XX (IDEC-) IDEC PHARM CORP.
XX Braslawsky GR, Hanna N, Chinn P;
XX WPI; 2002-698547/75.
XX N-ESDB; RAD45755.
XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
XX -72, or C2B8 antibody reactive with CD20, useful for treating
XX myelosuppressed patient suffering from a neoplastic disorder.
XX Example 2; Fig 4A; 74pp; English.

The present invention relates to domain deleted CC49 or C2B8 antibodies.
Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
deleted sequence in which CH2 domain has been deleted and are reactive
with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
with CD20 and comprise a heavy chain having a sequence of a derived
domain deleted C2B8 construct where the CH2 domain has been deleted.
Sequences of the invention are useful for imaging a neoplasm. They are
also useful for treating myelosuppressed patients suffering from
neoplastic disorder such as haematologic neoplasm, preferably non-
Hodgkin's lymphoma. Antibodies of the invention are also used to treat

CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human CH2 domain deleted CC49 antibody
 CC heavy chain protein. This sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 354 AA;

Query Match 100.0%; Score 1876; DB 5; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.1e-114;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60
 DB 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60
 QY 61 GQRLWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLN 120
 DB 61 GQRLWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLN 120
 QY 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSGTAAALGCLVKDYPEPVTVMNSGAL 180
 DB 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSGTAAALGCLVKDYPEPVTVMNSGAL 180
 QY 181 TSGVHTTTPAVLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKT 240
 DB 181 TSGVHTTTPAVLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKT 240
 QY 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 DB 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 QY 301 TTPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354
 DB 301 TTPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354

RESULT 2
 ABB82835
 ID ABB82835 standard; protein; 354 AA.
 XX
 AC ABB82835;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Antibody huCC49 CH2 domain deleted heavy chain.
 XX
 CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
 KW neuroprotective; antiporiatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN WO200296948-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-JAN-2002; 2002WO-US002374.
 XX
 PR 29-JAN-2001; 2001US-0264318P.
 PR 16-NOV-2001; 2001US-0331481P.
 PR 21-DEC-2001; 2001US-0341858P.
 XX
 FA (IDEC-) IDEC PHARM CORP.
 XX
 PI Braeslawsky GR, Hanna N, Chinn P, Hariharan K;
 XX
 DR WPI; 2003-140446/13.
 DR N-PSDB; ABZ24019.
 XX

PT Novel dimeric antibody useful for treating immune disorder and neoplastic
 disorder, has several non-covalently associated monomeric subunits.
 XX
 PS Example 1; Fig 4A; 78pp; English.
 XX
 CC- The invention relates to a dimeric antibody (I) comprising several
 monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
 CC detailed description of the various uses of (I)). The present sequence
 CC represents the antibody huCC49 CH2 domain deleted heavy chain
 XX
 SQ Sequence 354 AA;

Query Match 100.0%; Score 1876; DB 6; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.1e-114;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60
 DB 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHVKQNP 60
 QY 61 GQRLWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLN 120
 DB 61 GQRLWIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLN 120
 QY 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSGTAAALGCLVKDYPEPVTVMNSGAL 180
 DB 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSGTAAALGCLVKDYPEPVTVMNSGAL 180
 QY 181 TSGVHTTTPAVLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKT 240
 DB 181 TSGVHTTTPAVLQSSGLYSLSVTVPSSSLGTQYICNVNHPKSNTKVDKVEPKSCDKT 240
 QY 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 DB 241 HTCPPCPGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 QY 301 TTPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354
 DB 301 TTPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 354

RESULT 3
 AAE27924
 ID AAE27924 standard; protein; 360 AA.
 XX
 AC AAE27924;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human CH2 domain deleted C2B8 protein.
 XX
 KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
 KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
 KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200260955-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 29-JAN-2002; 2002WO-US002373.

C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer; dermatological; immunosuppressive; antiinflammatory.

Homo sapiens.
WO200296948-A2.
05-DEC-2002.
29-JAN-2002; 2002WO-US002374.
29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
(IDEC-) IDEC PHARM CORP.
Braslawsky GR, Hanna N, Chinn P, Hariharan K;
WPI; 2003-140446/13.
N-PSDB; ABZ24017.

Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
Example 1; Fig 1B; 78pp; English.

The invention relates to a dimeric antibody (I) comprising several monomeric subunits, where the monomeric subunits are non-covalently associated. (I) is useful for treating a disorder, especially immune disorder, and neoplastic disorder such as relapsed Hodgkin's disease, resistant Hodgkin's disease high grade, low grade and intermediate grade non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL), lymphoplasmacytoid lymphoma (LP), mantle cell lymphoma (MCL), follicular lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma, AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic lymphadenopathy, small lymphocytic, follicular, diffuse large cell, diffuse small cleaved cell, large cell immunoblastic lymphoblastoma, small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a detailed description of the various uses of I). The present sequence represents the antibody C2B8 CH2 domain deleted heavy chain

Sequence 360 AA;

Query Match 89.7%; Score 1683; DB 6; Length 360;
Best Local Similarity 88.6%; Pred. No. 4.5e-102;
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1

Qy 1 MGWSLLILLFLVAVATRVLSQVLVSGAEVVPKASVKISCKASGYTFTHAIHWKQP 60
Db 1 MGWSLLILLFLVAVATRVLSQVLVSGAEVVPKASVKISCKASGYTFTHAIHWKQP 60
Qy 61 GORLEWIGYFSPGNDPKNERFKGKATLTADTSASTAYVELSSLRSEDTAVYFCRSLN 120
Db 61 GRGLEWIGAIYPNGDTSYNQKFKGKATLTADKSSTAYVMQLSSLTSDSAVYYCARSTY 120
Qy 121 MA-----YWGQGTLVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPEPTVS 174
Db 121 YGGDWTFNVWGAGTTVTVAASKTGPSVPLAPSSKSTSGGTAALGCLVKDYFPPEPTVS 180
Qy 175 WNSGALTSGVHTFPVAVLQSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVVTPVSSSLGTQTYICNVNHKPSNTKVDKKVEP 240
Qy 235 KSCDKTKHTCPPCPGPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 294
Db 241 KSCDKTKHTCPPCPGPGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 300
Qy 295 ENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 354
Db 301 ENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 360

RESULT 4
ABB82833
ID ABB82833 standard; protein; 360 AA.
AC ABB82833;
XT 31-MAR-2003 (first entry)
DE Antibody C2B8 CH2 domain deleted heavy chain.

Qy 295 ENNYKTPPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
 Db 301 ENNYKTPPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 360

RESULT 5
 AAE27923
 ID AAE27923 standard; protein; 470 AA.
 AC AAE27923;
 XX
 XX
 DT 27-DEC-2002 (first entry)
 XX
 XX
 DE Human C2B8 antibody heavy chain protein.
 XX
 XX Human C2B8 antibody; tumour associated antigen; TAG-72;
 KW neoplasm; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
 KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
 KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200260955-A2.
 XX
 XX
 PD 08-AUG-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002373.
 XX
 XX 29-JAN-2001; 2001US-0264318P.
 XX
 PR 16-NOV-2001; 2001US-0331481P.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 FA
 XX
 XX Braslawsky GR, Hanna N, Chinn P;
 PI
 XX
 XX WPI; 2002-698547/75.
 DR N-PSDB; AAD45752.
 DR
 XX
 XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
 PT -72, or C2B8 antibody reactive with CD20, useful for treating
 PT myelosuppressed patient suffering from a neoplastic disorder.
 XX
 XX Example 1; Fig 1A; 74pp; English.
 PS
 XX
 XX The present invention relates to domain deleted CC49 or C2B8 antibodies.
 CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
 CC deleted sequence in which CH2 domain has been deleted and are reactive
 CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
 CC with CD20 and comprise a heavy chain having a sequence of a derived
 CC domain deleted C2B8 construct where the CH2 domain has been deleted.
 CC Sequences of the invention are useful for imaging a neoplasm. They are
 CC also useful for treating myelosuppressed patients suffering from
 CC neoplastic disorder such as haematologic neoplasm, preferably non-
 CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
 CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human C2B8 heavy chain protein. This
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 470 AA;
 SQ

Query Match 86.0%; Score 1614; DB 5; Length 470;
 Best Local Similarity 67.7%; Pred. No. 2e-97;
 Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTDTDAIHVKQNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTDTSYNMHWKQTP 60

Qy 61 QORLEWIGYFPGNDFFKYNRFKGAATLTADTASTAYVELSSLRSDTAVYFCTSLN 120
 Db 61 GRGLEWIGAIYFGNGDTSYNQKFGKATLTADKSSSTAYMQLSLTSDSAVYICARSTY 120

Qy 121 MA-----YNGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YGSDWYFNWAGAGTTVTVAASTKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180

Qy 175 WNSGALTSGVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKVEP 234
 Db 181 WNSGALTSGVHTTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKAEP 240

Qy 235 KSCDKTHTCPPCP----- 247
 Db 241 KSCDKTHTCPPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
 Db 301 YVDCGEVHNAKTRPRERQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

Qy 248 ---GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESGQPNNTKTPPV 304
 Db 361 KAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESGQPNNTKTPPV 420

Qy 305 LDSGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
 Db 421 LDSGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

RESULT 6
 ABB82832
 ID ABB82832 standard; protein; 470 AA.
 XX
 AC ABB82832;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Antibody C2B8 heavy chain.
 XX
 XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiaesthematic;
 KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thymimetic; hepatotropic; haemostatic; antileptotic; antibacterial;
 KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX WO200296948-A2.
 PN
 XX
 XX 05-DEC-2002.
 PD
 XX
 XX 29-JAN-2002; 2002WO-US002374.
 CC
 XX 29-JAN-2001; 2001US-0264318P.
 PR 16-NOV-2001; 2001US-0331481P.
 PR 21-DEC-2001; 2001US-0341858P.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 DA
 XX
 XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
 PI
 XX
 XX WPI; 2003-140446/13.
 DR
 DR N-PSDB; ABZ24016.
 XX
 PT Novel dimeric antibody useful for treating immune disorder and neoplastic
 PT disorder, has several non-covalently associated monomeric subunits.
 XX
 XX Example 1; Fig 1A; 78pp; English.
 PS
 XX The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,

CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal. (i) is also useful for
CC treating allergic rhinitis, autoimmune haemolytic anemia, allergic
CC contact dermatitis, Addison's disease, atopic dermatitis, amyloidosis,
CC aplastic anemia, arteritis, asthma, ataxia-telangiectasia, autoimmune
CC oophoritis, Burger's disease, bronchitis, candidiasis, post-myocardial
CC infarction syndrome, carditis, celiac sprue, Chagas's disease, Chediak-
CC Higashi syndrome, Crohn's disease, cryoglobulinemia, diabetes mellitus,
CC erythema multiforme, glomerulonephritis, Goodpasture's syndrome, Grave's
CC disease, Hashimoto's thyroiditis, haemolytic disease of the newborn,
CC hepatitis, idiopathic thrombocytopenic purpura, leprosy, Lyme disease,
CC multiple sclerosis, myasthenia gravis, polymyositis, scleroderma,
CC paroxysmal nocturnal haemoglobinuria, psoriasis, Raynaud's phenomenon/
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, systemic lupus
CC erythematosus, transplant rejection, and ulcerative colitis. (i) is also
CC useful for inducing hyper-cross-linking of membrane antigens, for killing
CC or inhibiting selected cell populations in the treatment of diseases such
CC as cancer and immune disorders, for treating myelosuppressed or
CC myelocompromised patients, for inducing apoptosis in the target cell
CC population or effectively block cell surface receptors necessary for the
CC growth of neoplastic cells, in viral or bacterial neutralization, for
CC diagnostic imaging of tumours, and for reducing tumour size, inhibiting
CC tumour growth and/or prolonging the survival time of tumour-bearing
CC animals. The present sequence represents the antibody C2B8 heavy chain
XX
SQ Sequence 470 AA;

Query Match 86.0%; Score 1614; DB 6; Length 470;
Best Local Similarity 67.7%; Pred. No. 2e-97; Indels 116; Gaps 2;
Matches 318; Conservative 13; Mismatches 23;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQTP 60
QY 61 GQRLWIGYFPGNDDFKYNRPFKQKATLTADTSASTAYVELSLRSEDYAVYFTRSLN 120
Db 61 GRGLEWVGAILYFPGNDFTSYNQKFKQKATLTADTSASTAYVELSLRSEDYAVYCARSTY 120
QY 121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVTS 174
Db 121 YGGDWYFNVWGAGTTVTVAASKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKQVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP 240
QY 235 KSCDKTHTCPPCP----- 247
Db 241 KSCDKTHTCPPCPAPPELLGPGSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
Db 301 YVDGVEVNAKTPREBQYNSTYRVSVLTVLHQDLNKGKEYCKVSKNALPAPTEKISKAK 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 354
Db 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470

RESULT 7
AAW52156
ID AAW52156 standard; protein; 731 AA.
XX
AC AAW52156;
XX

DT 05-FEB-2002 (first entry)
XX Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
DE
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX Homo sapiens.
OS Synthetic.
XX WO200174905-A1.
PN 11-OCT-2001.
PD
XX 26-MAR-2001; 2001WO-GB001324.
XX 03-APR-2000; 2000GB-00008049.
PR 02-OCT-2000; 2000US-0237159P.
XX (ANTI-) ANTISOMA RES LTD.
XX Young RJ;
PI WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanized monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity.
XX Claim 20; Fig 7; 176pp; English.
XX The invention relates to a compound which comprises a target cell-
CC specific portion, comprising a humanised monoclonal antibody, having
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC fragment and a cytotoxic portion having endonucleolytic activity.
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis
XX Sequence 731 AA;

Query Match 86.0%; Score 1613.5; DB 4; Length 731;
Best Local Similarity 67.7%; Pred. No. 3.5e-97;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNHWQAP 60
QY 61 GQRLWIGYFPGNDDFKYNRPFKQKATLTADTSASTAYVELSLRSEDYAVYFTRSLN 120
Db 61 GRGLEWVGAILYFPGNDFTSYNQKFKQKATLTADTSASTAYVELSLRSEDYAVYCARSYD 120
QY 121 ---MAYWQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVTSWNS 177
Db 121 FAWFAWQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVTSWNS 180
QY 178 GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKQVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKQVEPKSC 240
QY 238 DKTHTCPPCP----- 247
Db 241 DKTHTCPPCPAPPELLGPGSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYVD 300
QY 248 ----- 247
Db 301 GVEVHNAKTPREBQYNSTYRVSVLTVLHQDLNKGKEYCKVSKNALPAPTEKISKAK 360
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420

polypeptide. The dimeric immunoglobulin is used in the method of the invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically engineering a monoclonal antibody to introduce a cysteine molecule which inhibits formation of intramolecular disulphide bridges between sister heavy chains on the same antibody molecule. The dimer is a homodimer or heterodimer that is capable of activating components of the complement system, and has the ability to activate and kill cells via the complement cascade. The dimer is also capable of binding to Fc gamma receptors on cytotoxic effector cells and on host immune cells, and is capable of initiating programmed cell death. The IgG/IgG dimers may be used to treat allergic disorders, cancers and autoimmune diseases such as allergic asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food allergies, allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 470 AA;

Query Match 86.0%; Score 1613; DB 3; Length 470;
 Best Local Similarity 67.7%; Pred. No. 2.3e-97;
 Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKVKNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNHWVKTP 60

Qy 61 GQRLWIGYFSPGNDDFKYNRFKGTATLTADTSASTAYVELSLRSRSDTAVYFCTRSLN 120
 Db 61 GRGLEWIGALYPGNGDTSYNOKFKGKATLTADKSSSTAYMQLSLSLTSRSDSAVYICARSTY 120

Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 174
 Db 121 YGGDWYFNVWGAGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180

Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEP 234
 Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEP 240

Qy 235 KSDKTHTCPPCP----- 247
 Db 241 KSDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Qy 248 ----- 247

Db 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
 Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420

Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 354
 Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPGK 470

RESULT 10
 AAM52158
 ID AAM52158 standard; protein; 729 AA.
 XX
 AC AAM52158;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
 XX
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX Homo sapiens.
 OS Synthetic.
 XX WO200174905-A1.
 XX 11-OCT-2001.
 XX 26-MAR-2001; 2001WO-GB001324.
 XX 03-APR-2000; 2000GB-00008049.
 PR 02-OCT-2000; 2000US-0237159P.
 XX (ANTI-) ANTISOMA RES LTD.
 XX Young RJ;
 WIPI; 2001-662969/76.
 Novel compound used to treat cancer has target cell-specific portion comprising humanized monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity.

XX Claim 20; Fig 9; 176pp; English.

XX The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity. The compound is exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis

XX SQ Sequence 729 AA;

Query Match 85.7%; Score 1608.5; DB 4; Length 729;
 Best Local Similarity 67.6%; Pred. No. 7.5e-97;
 Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKVKNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFSAYWIEWRQAP 60

Qy 61 GQRLWIGYFSPGNDDFKYNRFKGTATLTADTSASTAYVELSLRSRSDTAVYFCTRSLN 120
 Db 61 GKGLEWVGEILPGSNNSRYNEKFKGRVTVTRDTSTNTAYMBELSLRSRSDTAVYICARSYD 120

Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNS 177
 Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNS 180

Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSC 237
 Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSC 240

Qy 238 DKTHTCPPCP----- 247
 Db 241 DKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300

Qy 248 ----- 247

Db 301 GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360

Qy 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 307
 Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 420

Qy 308 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPG 353
 Db 421 DGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSPG 466

[illegible]

XX New antibodies and proteins bind conserved epitope of Fas antigen - used
PT to evaluate drugs in animal models and to treat Fas-associated diseases
PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
XX hepatitis and AIDS.
XX
PS Claim 22; Page 212-213; 292pp; English.
XX
CC This is the amino acid sequence of the VD type humanised heavy chain of
CC murine anti-human Fas monoclonal antibody HFE7A. E. coli pGSHSL7A62 SANK
CC 73397 harbors plasmid pGSHSL7A62 carrying a fusion fragment of the
CC humanised VD type HFE7A heavy chain and DNA encoding human IgG1 constant
CC region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The
CC invention provides methods for producing humanised antibodies by
CC culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like
CC native HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells.
CC The humanised antibodies are used to evaluate, in animal models,
CC treatments of diseases that involve Fas/Fas ligand interactions, and also
CC to treat such diseases, including autoimmune disease (e.g. systemic lupus
CC erythematosus, Hashimoto's disease, graft versus host disease, Sjogren
CC syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture
CC syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic
CC anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's
CC disease, thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection
CC (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 470 AA;

Query Match 85.4%; Score 1603; DB 2; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASYTFTDTHAIHWKQNP 60
1 MGWSLILFLVATATGTVHSGVQLVQSGAEVVKPGASVKISKASYTFTSYMQWVKQAP 60
61 GQRLWIGYFSGNDPDFKNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLN 120
61 GQRLWIGYFSGNDPDFKNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLN 120
121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
175 WNSGALTSVGHVTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 234
181 WNSGALTSVGHVTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 240
235 KSCDKTHCTPCP----- 247
241 KSCDKTHCTPCPAPPELLGGPSVFLFPPKPTLMISRTPEVTCVVDVSHEDPEVKFNW 300
248 ----- 247
301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDLNGLKEKCKVSKNALPAPIEKTIS 360
248 --GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
361 KAKGQPREPQVYTLPPSRDEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
305 LDSGGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNYHTQKLSLSFGK 354
421 LDSGGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNYHTQKLSLSFGK 470
RESULT 13
AAB14776
ID AAB14776 standard; protein; 470 AA.
XX
AC AAB14776;

XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
KW humanised antibody; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; heavy chain.
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX JP2000169393-A.
XX 20-JUN-2000.
XX 30-SEP-1999; 99JP-00278301.
XX 30-SEP-1998; 98JP-00276883.
XX (SANY) SANKYO CO LTD.
XX WPI; 2000-485645/43.
DR N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality in
PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
PT antibody.
PS Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment or
CC diseases caused by an abnormality in the Fas/Fas ligand system containing
CC an anti-Fas antibody as the active component. The anti-Fas antibody is
CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
CC humanised version of HFE7A containing identical CDRs (complementarity
CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
CC antibody of the invention acts as a modulator of apoptosis. The
CC compositions of the invention may therefore be used in the treatment or
CC prevention of conditions such as autoimmune diseases, allergy, atopy,
CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
CC rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy
CC chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas
CC antibodies. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 470 AA;
Query Match 85.4%; Score 1603; DB 3; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASYTFTDTHAIHWKQNP 60
1 MGWSLILFLVATATGTVHSGVQLVQSGAEVVKPGASVKISKASYTFTSYMQWVKQAP 60
61 GQRLWIGYFSGNDPDFKNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLN 120
61 GQRLWIGYFSGNDPDFKNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLN 120
121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
175 WNSGALTSVGHVTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 234
181 WNSGALTSVGHVTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 240
XX

QY 235 KSCDKTHTCP- 247
 DB 241 KSCDKTHTCP- 300
 QY 248 - 247
 DB 301 YVDGVEVNAKTPREQYNSYRVRVSVLTVLHODWLNKGYCKVKVSNKALPAIEKTTIS 360
 QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPV 304
 DB 361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPV 420
 QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNNHYTKQSLSPGK 354
 DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNNHYTKQSLSPGK 470

RESULT 14

AAW90926
 ID AAW90926 standard; protein; 470 AA.

AC AAW90926;

DT 08-AUG-2000 (first entry)

DE Humanised HFE7A designed heavy chain protein.

QY Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; infertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-00307711.

XX 30-SEP-1998; 98JP-00276881.

XX 30-SEP-1998; 98JP-00276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11597.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems.

XX Example reference 15; Page 134-136; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between
 XX Fas and its ligand. The products of the invention have anti-inflammatory,
 XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 XX immunomodulatory, dermatological, immunosuppressive, thymimetic,
 XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 XX antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 XX apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention

XX SQ Sequence 470 AA;

Query Match 85.4%; Score 1603; DB 3; Length 470;

Best Local Similarity 67.0%; Pred. No. 1e-96;

Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKVPGASVKISKASGYTFTDHAHHWKNP 60

DB 1 MGWSLILFLVATATGVHSQVLVQSGAEVVKVPGASVKISKASGYTFTSYWQWVKQAP 60

QY 61 GORLEWGYSPGNDDFKYNRFKATLTADTSASTAYVELSLRSDETAVFCTSLN 120

DB 61 GORLEWMBGIDPDSYNTYNNQKFKATLTVDTSASTAYVELSLRSDETAVYYCARNRD 120

QY 121 MA-----YMGQGTFLVTVSSASTKPSVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVS 174

DB 121 YSNWNYFDVWGEGLTVTVSSASTKPSVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVS 180

QY 175 WNSGALSGVHTFPAPVLOSGLYSLSVTVVPSSSLGTQTYICNNHKKPSNTKVDKKVEP 234

DB 181 WNSGALSGVHTFPAPVLOSGLYSLSVTVVPSSSLGTQTYICNNHKKPSNTKVDKKVEP 240

QY 235 KSCDKTHTCP- 247

DB 241 KSCDKTHTCP- 300

QY 248 - 247

DB 301 YVDGVEVNAKTPREQYNSYRVRVSVLTVLHODWLNKGYCKVKVSNKALPAIEKTTIS 360

QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPV 304

DB 361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTTPPV 420

QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNNHYTKQSLSPGK 354

DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVMEALHNNHYTKQSLSPGK 470

RESULT 15

ABB74941

ID ABB74941 standard; protein; 470 AA.

XX ABB74941;

XX 30-APR-2002 (first entry)

DT Humanised anti-Fas antibody light chain SEQ ID NO 50.

DE Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;

KW heavy chain; apoptosis; anti-allergic; immunosuppressive; apoptotic;

KW autoimmune disease; allergy; atopy.

XX Synthetic.

OS

XX

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FN JP2001342149-A.
XX
PD 11-DEC-2001.
XX
PF 28-MAR-2001; 2001JP-00093243.
XX
PR 29-MAR-2000; 2000JP-00091144.
XX
PA (SANY ) SANKYO CO LTD.
XX
DR WPI; 2002-145114/19.
XX
DR N-PSDB; ABL48674.
XX
PT Drug for preventing or treating e.g. autoimmune disease or allergy,
PT comprises humanized anti-Fas antibody.
XX
PS Example 14 (preparatory); Page 79; 154pp; Japanese.
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in the Fas/Fas ligand system containing, as the
CC active component, an antibody having a light chain subunit and a heavy
CC chain subunit and an activity of combining specifically with mammalian
CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
CC agent has antiallergic, immunosuppressive and apoptotic activity and is
CC used for preventing and treating autoimmune diseases, allergy, atopy and
CC others
XX
SQ Sequence 470 AA;
Query Match 85.4%; Score 1603; DB 5; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
Qy 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Db 1 MGWSLILFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Qy 61 GORLEWIGYFSPGNDFFKYNREKFKATLTADTSASTAYVELSLRSEDYVYFCTRLN 120
Db 61 GORLEWMEIDPSYNTYNQKFKGATLTVDTSASTAYMELSLRSEDYVYFCARNRD 120
Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVS 174
Db 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVS 180
Qy 175 WNSGALTSQVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYDKVEP 234
Db 181 WNSGALTSQVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYDKVEP 240
Qy 235 KSCDKTHTCPCP----- 247
Db 241 KSCDKTHTCPCPAPPELLGSPSVFLFPPKPKDTLMSRTPEVTCVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIIS 360
Qy 248 ---GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

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Search completed: March 23, 2005, 18:34:43
Job time : 144.455 secs

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Qy 248 -----G 248
Db 301 VEVHNAKTPREEQYNSTRVVSVLTLVHQLDNLGKEYCKVSNKALPAPIETKTSKAG 360
Qy 249 QPREPOVTLPSRDELTKNOVSLTCLVKGYPSPDIAVWESNGQPNENYKTTTPVLDS 308
Db 361 QPREPOVTLPSREEMTKNOVSLTCLVKGYPSPDIAVWESNGQPNENYKTTTPVLDS 420
Qy 309 GSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSLSPGK 354
Db 421 GSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSLSPGK 466
RESULT 2
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chessa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 82.6%; Score 1549; DB 4; Length 472;
Best Local Similarity 65.3%; Pred. No. 4.6e-111; Indels 120; Gaps 3;
Matches 309; Conservative 15; Mismatches 29;
Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Db 1 MDWTWRVFLCLAVAPGAHSQVQLVQSGAEVVKPGASVKISCTSYTFETIHWVQAP 60
Qy 61 GQRLWIGYFSPGNDFFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTR--- 117
Db 61 GQRLWIGGINPNNGIPNINQKFGKATLTGVKASASTAYVELSLRSEDVAVYFCARRI 120
Qy 118 -----SLNMAVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVADYFPEPV 171
Db 121 AYGDEGHAMDYWGQGLTVTVSS--STKGPSVFPLAPSKSTSGGTAALGCLVADYFPEPV 179
Qy 172 TVSNWNGALTSGVHTFPFPAVLQSSGLYSLSSVTVTPVSSSLGTQTYICNVNHPKSNTKVDKK 231
Db 180 TVSNWNGALTSGVHTFPFPAVLQSSGLYSLSSVTVTPVSSSLGTQTYICNVNHPKSNTKVDKK 239
Qy 232 VEPKSCDKTHTCPCPCP----- 247
Db 240 VEPKSCDKTHTCPCPCPAPPELLAGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 299
Qy 248 ----- 247
Db 300 FNTWYDGVENVAKTKPREEQYNSTRVVSVLTVLHQLDNLGKEYCKVSNKALPAPIEK 359
Qy 248 -----GQPREPOVTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNGQPNENYKTT 301
Db 360 TISKAKGQPREPOVTLPPSRDELTKNOVSLTCLVKGYPSPDIAVWESNGQPNENYKTT 419
Qy 302 PPVLDSGSGFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSLSPGK 354

Db 420 PPVLDSGSGFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSLSPGK 472
RESULT 3
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13

Query Match 82.1%; Score 1541; DB 1; Length 449;
Best Local Similarity 67.5%; Pred. No. 1.8e-110;
Matches 303; Conservative 10; Mismatches 22; Indels 114; Gaps 2;
Qy 20 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNPGRLEWIGYFSPGNDFFKY 79
Db 1 QVQLVQSGAEVVKPGASVKISKASGYAFTNYLIEWRQAPGQGLEWIGYVPGSGGTNY 60
Qy 80 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTRSLN---MAYWGQGLTVTVSSA 135
Db 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTRSLN---MAYWGQGLTVTVSSA 120
Qy 136 STKGPSVFPLAPSKSTSGGTAALGCLVADYFPEPVTVSNWNGALTSGVHTFPFPAVLQSSG 195
Db 121 STKGPSVFPLAPSKSTSGGTAALGCLVADYFPEPVTVSNWNGALTSGVHTFPFPAVLQSSG 180
Qy 196 LYSLSVSVTVTPVSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPCP----- 247
Db 181 LYSLSVSVTVTPVSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPCPAPPELLGGP 240
Qy 248 ----- 247
Db 241 SVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVENVAKTKPREEQYNS 300

Qy 248 -----GOPREPOVYTLPPSRDEL 265
Db 301 TYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Qy 266 TKNQVSLTCLVKGFYPSDIAWVEESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 325
Db 361 TKNQVSLTCLVKGFYPSDIAWVEESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
Qy 326 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
RESULT 4
US-09-301-593-30
; Sequence 30, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-30
Query Match 81.2%; Score 1524; DB 4; Length 472;
Best Local Similarity 63.8%; Pred. No. 3.8e-109;
Matches 302; Conservative 20; Mismatches 31; Indels 120; Gaps 3;
Qy 1 MGWSLILLFLVAVATRYLSQVQLVQSGAEVVKPGASVKISKASGYFTTDAIHVVKQNP 60
Db 1 MGWSVFLFLSGTAGVLSVQLQSGPELVKPGASVKMSCKTSRYTFTETIHWVRQSH 60
Qy 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSLRSEDATVYFCTR--- 117
Db 61 GKSLEWIGGINPNNGIPNYPKGRATLTVGKSSSTAYMEIRSLTSDSAVYFCARRRI 120
Qy 118 -----SLNMAWYGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 171
Db 121 AYGDEGHAMDYWGQTSVTVSS-STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 179
Qy 172 TVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKK 231
Db 180 TVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKK 239
Qy 232 VEPKSCDKTHTCPCPCP----- 247
Db 240 VEPKSCDKTHTCPCPCPELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVK 299
Qy 248 ----- 247
Db 300 FNTYVDGVEVHNAKTPREEQYNTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 359
Qy 248 -----GOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWVEESNGQPENNYKTT 301
Db 360 TISKAKGQPREPQVYTLPPSRDEEMTKNQVSLTCLVKGFYPSDIAWVEESNGQPENNYKTT 419
Qy 302 PPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

Db 420 PPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472
RESULT 5
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS: 46
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; NAME: ERNST, BARBARA G
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10
Query Match 80.3%; Score 1506; DB 2; Length 476;
Best Local Similarity 63.4%; Pred. No. 9.3e-108;
Matches 302; Conservative 20; Mismatches 32; Indels 122; Gaps 3;
Qy 1 MGWSLILLFLVAVATRYLSQVQLVQSGAEVVKPGASVKISKASGYFTTDAIHVVKQNP 60
Db 1 MDWTRFLVVAATQVQSQVQVQSGAEVVKPGSSVTVSCASGGTFSNVAISWRQAP 60
Qy 61 GQRLWIGYFSPGNDDFKYNRFKPKATLTADTSASTAYVELSLRSEDATVYFCT--- 116
Db 61 GQGLEWNGGIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDATVYCATDRI 120
Qy 117 RSLNMAWY-----WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 168
Db 121 RQAFDRAVGVDFPQWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
Qy 169 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 228
Db 181 EPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 240
Qy 229 DKKVEPKSCDKTHTCPCPCP----- 247
Db 241 DKKVEPKSCDKTHTCPCPCPELLGGPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDP 300
Qy 248 ----- 247


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; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma
; TITLE OF INVENTION: CACHEXIA, IMMUNO
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09485737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/BP 98/
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 988701
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 978701
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

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Query Match 80.0%; Score 1501; DB 3; Length 711;
Best Local Similarity 63.8%; Pred. No. 3.7e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 11

Qy	6	ILFLVAVATRVLSQVOLVGSGAEVVPKGASVKISCKASGYTFTHDAIHWVKQNPQGRLE	65
Db	7	IFGFLAISVILLSQVOLVGSGSELKKGASVKISCKASGYTFDYGNNVWKQAPGQGLK	66
Qy	66	WIGVFSQGNDDFKNERPKGKATLTADTASTAVELSSLRSEDTAVYFCTRS--LNNAY	123
Db	67	WMGWINYTGESTYVDGKGFPSLDTISVAAVLQISSUKAEDATYFCARRGFYAMDY	126
Qy	124	WGQGLTVTSASASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPEPPTVSNWSGALTSG	183
Db	127	WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPEPPTVSNWSGALTSG	186
Qy	184	VHTFPVLQSSGLYSLSVTVTPSSLSGTQTYICNVNHNKPSNTKVDKVBKPSCKDKTHTC	243
Db	187	VHTFPVLQSSGLYSLSVTVTPSSLSGTQTYICNVNHNKPSNTKVDKVBKPSCKDKTHTC	246
Qy	244	PPCP-----	247
Db	247	PPCPAPELLGGPSVFLPPPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	306
Qy	248	-----	253
Db	307	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIETKISKARGQPREP	366
Qy	254	QVYTLPPSRBELTKNOVSLNCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFEL	313
Db	367	QVYTLPPSRBEMTKNOVSLNCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFPL	426
Qy	314	YSKLTVDKSRWQGNVFCSCVMHEALNHYTKQSLSLSPGK	354
Db	427	YSKLTVDKSRWQGNVFCSCVMHEALNHYTKQSLSLSPGK	467

RESULT 9

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US-10-071-485-90
; Patent No. 63071485
; Sequence No. 630752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma
; TITLE OF INVENTION: SHOCK
; TITLE OF INVENTION: CACHEXIA, IMMUNO

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; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

```

Query Match	80.0%;	Score 1501;	DB 4;	Length 711;
Best Local Similarity	63.8%;	Pred. No. 3.7e-107;		
Matches 294; Conservative	24;	Mismatches 31;	Indels 112;	Gaps 2;

Qy	6	ILLFLVAVATRVLSQVQLVSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPGRLE	65
Db	7	IFSFLISASVILSQVQLVSGSELKPGASVKISKASGYTFTDYGNNVWKQAPGGCLK	66
Qy	66	WIGVFSPGNDDFKYNRERFKCATLTADTASTAVVELSSRSEDYAVVFCTRS--LNWAY	123
Db	67	WMGWINTYTGESTYVDDFKGRFVPSLDTVSAAVLIQISSLKAEDETATYFCARRGFYAMDY	126
Qy	124	WGOGTLTVTVSSASTKGPSVFPEPLAPSSKSTSGGTAALGCLVKDYPPETVTVSNWSGALTSG	183
Db	127	WGOGTTTVTVSSASTKGPSVFPEPLAPSSKSTSGGTAALGCLVKDYPPETVTVSNWSGALTSG	186
Qy	184	VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKRVKPKCDKTHTC	243
Db	187	VHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKRVKPKCDKTHTC	246
Qy	244	PPCP-----	247
Db	247	PPCPAPPELLGGPSVFLFPPPKDLMISRPTCVVVDVSHEDPEVKFNWYVDGVGVHN	306
Qy	248	-----GQPREP	253
Db	307	AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTTISKAKGQPREP	366
Qy	254	QVYTTLPSPRDLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGFFFL	313
Db	367	QVYTTLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGFFFL	426
Qy	314	YSKLTVDKSRWQQGVFSCSVMHEALHNHYTQKSLSLSPGK	354
Db	427	YSKLTVDKSRWQQGVFSCSVMHEALHNHYTQKSLSLSPGK	467

RESULT 10

```

US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE
; NUMBER OF SEQUENCES: 28

```

APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28


```

; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
US-09-627-896B-24

Query Match          79.2%; Score 1485; DB 4; Length 462;
Best Local Similarity 63.9%; Pred. No. 3.7e-106;
Matches 297; Conservative 21; Mismatches 33; Indels 114; Gaps 4;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db 1 MGWCIIFLVTATGHSQVQLVQSGAEVVKPGSSVKSKASGYTFTDVAIQWRQAP 60
Qy 61 GQRLWIGYFPGNDDFKYNRFKGTATLTADTSASTAYVELSLRSEDATVYFCTSL- 119
Db 61 GQGLEWIGVINIYDNTYINOKFKGATMTVDKSTSTAYMELSLRSEDATVYFCARA 120
Qy 120 NMAYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGA 179
Db 121 YMDYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGA 180
Qy 180 LTSGVHTPPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT-KVDKKVEPKSCD 238
Db 181 LTSGVHTPPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT-KVDKKVEPKSCD 240
Qy 239 KTHICPPCP----- 247
Db 241 E---CPPCPAPPAAPSVFLPPPKPKOTLMISRTPEVTCVVVDVSHEDPEVQFNMYVDGV 297
Qy 248 -----GQ 249
Db 298 EVHNKTKPREQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQ 357
Qy 250 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 309
Db 358 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 417
Qy 310 SFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
Db 418 SFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 462

RESULT 13
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street

```

```

; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-8

Query Match          79.2%; Score 1485; DB 3; Length 478;
Best Local Similarity 61.1%; Pred. No. 3.8e-106;
Matches 292; Conservative 25; Mismatches 37; Indels 124; Gaps 3;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db 1 MGWSLILFLVAVATRVQCEVQLVESGGLVQPGSLRVSCAVSGFTFSDHYMYPRQAP 60
Qy 61 GQRLWIGYF--SPGNDDFKYNRFKGTATLTADTSASTAYVELSLRSEDATVYFCTRS 118
Db 61 GKGPEWGFIRNRKNGGTTTAAASVKDRFTISRDDSKSIAYLQWSSLKIEDTAVYCYTS 120
Qy 119 L-----NMAYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 166
Db 121 YISHCRGVGVGCVGFYFEGWGGALVTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDY 180
Qy 167 FPEPTVYSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT 226
Db 181 FPEPTVYSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT 240
Qy 227 KVDKKVEPKSCDKTHHTCPCP----- 247
Db 241 KVDKKVEPKSCDKTHHTCPCPAPPELLGGPSVFLPPKPKOTLMISRTPEVTCVVVDVSH 300
Qy 248 ----- 247
Db 301 DPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296
Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Qy 297 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
Db 421 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 478

RESULT 14
US-09-526-098-8
; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

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Db 301 DPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
 Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296
 Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
 Qy 297 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHIALHNNHYTKLSLSPGK 354
 Db 421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHIALHNNHYTKLSLSPGK 478

Search completed: March 23, 2005, 18:35:50
 Job time : 39.3535 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:26:57 ; Search time 109.061 Seconds
(without alignments)
1074.721 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNHYTKLSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1613.5	86.0	731	9	US-09-825-012-46 Sequence 46, Appl
2	1613.5	86.0	741	9	US-09-825-012-55 Sequence 55, Appl
3	1608.5	85.7	729	9	US-09-825-012-52 Sequence 52, Appl
4	1608.5	85.7	739	9	US-09-825-012-61 Sequence 61, Appl
5	1603	85.4	470	14	US-10-216-484-89 Sequence 89, Appl
6	1603	85.4	470	14	US-10-384-933-89 Sequence 89, Appl
7	1602.5	85.4	730	9	US-09-825-012-49 Sequence 49, Appl
8	1602.5	85.4	740	9	US-09-825-012-58 Sequence 58, Appl
9	1595	85.0	470	14	US-10-216-484-143 Sequence 143, App
10	1595	85.0	470	14	US-10-384-933-143 Sequence 143, App
11	1593	84.9	470	14	US-10-216-484-145 Sequence 145, App
12	1593	84.9	470	14	US-10-384-933-145 Sequence 145, App
13	1592	84.9	470	14	US-10-216-484-117 Sequence 117, App

14	1592	84.9	470	14	US-10-216-484-147	Sequence 147, App
15	1592	84.9	470	14	US-10-384-933-117	Sequence 117, App
16	1592	84.9	470	14	US-10-384-933-147	Sequence 147, App
17	1579	84.2	470	14	US-10-216-484-157	Sequence 157, App
18	1579	84.2	470	14	US-10-384-933-157	Sequence 157, App
19	1565.5	83.4	467	14	US-10-171-452A-47	Sequence 41, Appl
20	1565.5	83.4	467	14	US-10-171-452A-47	Sequence 47, Appl
21	1565.5	83.4	467	14	US-10-171-452A-53	Sequence 53, Appl
22	1565.5	83.4	467	14	US-10-171-452A-53	Sequence 59, Appl
23	1565.5	83.4	467	15	US-10-353-708-41	Sequence 41, Appl
24	1565.5	83.4	467	15	US-10-353-708-47	Sequence 47, Appl
25	1565.5	83.4	467	15	US-10-353-708-53	Sequence 53, Appl
26	1565.5	83.4	467	15	US-10-353-708-59	Sequence 59, Appl
27	1565.5	83.4	467	16	US-10-731-984-7	Sequence 7, Appl
28	1565.5	83.4	467	16	US-10-731-984-15	Sequence 15, Appl
29	1565.5	83.4	467	16	US-10-731-984-23	Sequence 23, Appl
30	1565.5	83.4	467	16	US-10-731-984-31	Sequence 31, Appl
31	1559.5	83.1	448	15	US-10-378-567-2	Sequence 2, Appl
32	1559	83.1	466	17	US-10-937-046-11	Sequence 11, Appl
33	1549	82.6	472	9	US-09-301-593-43	Sequence 43, Appl
34	1549	82.6	472	14	US-10-159-006-43	Sequence 43, Appl
35	1546.5	82.4	446	17	US-10-822-300-119	Sequence 119, App
36	1546.5	82.4	446	17	US-10-822-300-120	Sequence 120, App
37	1546	82.4	476	9	US-09-747-669-3	Sequence 3, Appl
38	1546	82.4	476	14	US-10-290-703-3	Sequence 3, Appl
39	1545.5	82.4	465	15	US-10-404-724-25	Sequence 25, Appl
40	1545.5	82.4	465	17	US-10-816-276-21	Sequence 21, Appl
41	1543.5	82.3	446	17	US-10-822-300-121	Sequence 121, App
42	1543.5	82.3	446	17	US-10-822-300-122	Sequence 122, App
43	1543.5	82.3	448	14	US-10-171-452A-42	Sequence 42, Appl
44	1543.5	82.3	448	14	US-10-171-452A-48	Sequence 48, Appl
45	1543.5	82.3	448	14	US-10-171-452A-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825.012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match	86.0%;	Score	1613.5;	DB 9;	Length	731;
Best Local Similarity	67.7%;	Pred. No.	1.3e-101;			
Matches	316;	Conservative	18;	Mismatches	20;	Indels 113; Gaps 2;
Qy	1	MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDRAIHVKNP	60			
Db	1	MGWSLILFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFTSAIEWVRQAP	60			
Qy	61	QORLEWIGYFSGNDPDFKYNRFRKQATLTADTASATAYVELSLRSDDTAVYFCTRSIN	120			
Db	61	CKGLEWGEIILPGSNSEYNEKFKGRVTVTDTSTNTAYMELSLRSDDTAVYCARSD	120			

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Qy 121 ---MAYWQGGTLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWPAYWGQGLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 354
Db 421 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 467

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RESULT 2

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US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-55

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Query Match 86.0%; Score 1613.5; DB 9; Length 741;
Best Local Similarity 67.7%; Pred. No. 1.4e-101;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Db 1 MGWSLILLFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFTSAYWIEWVRQAP 60
Qy 61 GQRLWIGYFSPGNDDFKYNRERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GKGLEWVGSEILPGNNRNYNEKFGKRVTVTRDTSTNTAYMELSLRSEDVAVYCARSD 120
Qy 121 ---MAYWQGGTLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWPAYWGQGLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300

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Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 354
Db 421 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 467

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RESULT 3

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US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

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Query Match 85.7%; Score 1608.5; DB 9; Length 729;
Best Local Similarity 67.6%; Pred. No. 2.9e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Db 1 MGWSLILLFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFTSAYWIEWVRQAP 60
Qy 61 GQRLWIGYFSPGNDDFKYNRERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GKGLEWVGSEILPGNNRNYNEKFGKRVTVTRDTSTNTAYMELSLRSEDVAVYCARSD 120
Qy 121 ---MAYWQGGTLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWPAYWGQGLVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKNTKVDKKEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 353
Db 421 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTKQSLSPGK 466

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RESULT 4

US-09-825-012-61
 ; Sequence 61, Application US/09825012
 ; Patent No. US20020122798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Robert
 ; TITLE OF INVENTION: Compounds for Targeting
 ; FILE REFERENCE: 43191-258808
 ; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 0008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 61
 ; LENGTH: 739
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
 ; US-09-825-012-61

Query Match 85.7%; Score 1608.5; DB 9; Length 739;
 Best Local Similarity 67.6%; Pred. No. 3e-101;
 Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;
 Qy 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHIVKQNP 60
 Db 1 MGWSLILFLVATATGVHSQVQVQSGAEVVKPGASVKISKASGYTFTDHAHIVKQNP 60
 Qy 61 GORLEWIGYFPGNDDFKYNRFRFGKATLTADTASTAYVELSLRSEDYAVYFCTRSN 120
 Db 61 GKLEWVGEILPGSNNSRYNEKFGRTVTTRDTSTNTAYMELSLRSEDYAVYCARSD 120
 Qy 121 ---MAYWQGTIVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 177
 Db 121 FAWFAYWQGTIVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 180
 Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVPKSC 237
 Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVPKSC 240
 Qy 238 DKHTCTPCPP----- 247
 Db 241 DKHTCTPCPPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 300
 Qy 248 ----- 247
 Db 301 GVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
 Qy 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 307
 Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 420
 Qy 308 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 353
 Db 421 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 466

RESULT 5

US-10-216-484-89
 ; Sequence 89, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/216,484
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 89
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
 ; OTHER INFORMATION: chain of humanized anti-Fas antibody
 ; US-10-216-484-89
 Query Match 85.4%; Score 1603; DB 14; Length 470;
 Best Local Similarity 67.0%; Pred. No. 4.2e-101;
 Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
 Qy 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHIVKQNP 60
 Db 1 MGWSLILFLVATATGVHSQVQVQSGAEVVKPGASVKISKASGYTFTSYMMQWVQAP 60
 Qy 61 GORLEWIGYFPGNDDFKYNRFRFGKATLTADTASTAYVELSLRSEDYAVYFCTRSN 120
 Db 61 GORLEWIGEIDPDSPTNYNOKFKGKATLTADTASTAYMELSLRSEDYAVYCARNRD 120
 Qy 121 MA-----YMQGTIVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 174
 Db 121 YSNWYFDVWGEGLTVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 180
 Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVPK 234
 Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVPK 240
 Qy 235 KSCDKHTCTPCPP----- 247
 Db 241 KSCDKHTCTPCPPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
 Db 361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
 Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 354
 Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 470
 RESULT 6
 US-10-384-933-89
 ; Sequence 89, Application US/10384933
 ; Publication No. US20030170817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030170817A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/384,933
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165


```
; SEQ ID NO 89
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-89

Query Match      85.4%; Score 1603; DB 14; Length 470;
Best Local Similarity 67.0%; Pred. No. 4.2e-101;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Qy 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 174
Db 121 YSNWYFDVWEGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180
Qy 175 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEVP 234
Db 181 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEVP 240
Qy 235 KSCDKHTCTPCPCP----- 247
Db 241 KSCDKHTCTPCPCPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Qy 248 ---GQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
Db 361 KAKGQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Qy 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 470

RESULT 7
US-09-825-012-49
; Sequence 49, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-49

Query Match      85.4%; Score 1602.5; DB 9; Length 730;
Best Local Similarity 67.5%; Pred. No. 7.5e-101;
Matches 314; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Qy 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 177
Db 121 FAWFAYWQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSC 240
Qy 238 DKTHCTPCPCP----- 247
Db 241 DKTHCTPCPCPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSP 352
Db 421 DGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSP 465

RESULT 8
US-09-825-012-58
; Sequence 58, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-58

Query Match      85.4%; Score 1602.5; DB 9; Length 740;
Best Local Similarity 67.5%; Pred. No. 7.6e-101;
Matches 314; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Qy 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDPFKYNRFGKATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 177
Db 121 FAWFAYWQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSC 240
Qy 238 DKTHCTPCPCP----- 247
Db 241 DKTHCTPCPCPELLGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSP 352
Db 421 DGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSP 465
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Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 11

US-10-216-484-145
 ; Sequence 145, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/216,484
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 145
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
 ; OTHER INFORMATION: chain of humanized anti-Fas antibody
 US-10-216-484-145

Query Match 84.9%; Score 1593; DB 14; Length 470;

Best Local Similarity 66.6%; Pred. No. 2e-100;
 Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
 Db 1 MGWSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISKASGYTFTSWMQWVKQAP 60
 Qy 61 GQRLWIGYFSGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDVAVYCTRLN 120
 Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDSTSTAYMELSLRSEDVAVYCARNRD 120
 Qy 121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YSNWYFDWQGGTLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180
 Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEP 234
 Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEP 240
 Qy 235 KSCDKHTCTCPCP----- 247
 Db 241 KSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNAKTPREQYNSYTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
 Db 361 KAKGQPREPQVYTLPPSRDEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 12

US-10-384-933-145

; Sequence 145, Application US/10384933
 ; Publication No. US200301070817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US200301070817A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/384,933
 ; PRIOR FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 145
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
 ; OTHER INFORMATION: chain of humanized anti-Fas antibody
 US-10-384-933-145

Query Match 84.9%; Score 1593; DB 14; Length 470;

Best Local Similarity 66.6%; Pred. No. 2e-100;
 Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
 Db 1 MGWSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISKASGYTFTSWMQWVKQAP 60
 Qy 61 GQRLWIGYFSGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDVAVYCTRLN 120
 Db 61 GQGLEWNGEIDPSDSTYNQKFGKATITVDSTSTAYMELSLRSEDVAVYCARNRD 120
 Qy 121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YSNWYFDWQGGTLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180
 Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEP 234
 Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKKVEP 240
 Qy 235 KSCDKHTCTCPCP----- 247
 Db 241 KSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNAKTPREQYNSYTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
 Db 361 KAKGQPREPQVYTLPPSRDEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 13

US-10-216-484-117
 ; Sequence 117, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru

```
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-117

Query Match      84.9%; Score 1592; DB 14; Length 470;
Best Local Similarity 66.6%; Pred. No. 2.4e-100;
Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
QY 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
DB 61 GQGLEWMMGEIDPSDSYTNYNQKFKGKATLTVDTTSTAYMELSLRSSEDTAVYFCARNRD 120
QY 121 MA-----YMGQGTLTAVTSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVTS 174
DB 121 YSNWNYFDVWEGTLTVTSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEP 234
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEP 240
QY 235 KSCDKHTCTCPCP----- 247
DB 241 KSCDKHTCTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
DB 361 KAKGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSFGK 354
DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSFGK 470

RESULT 15
US-10-384-933-117
; Sequence 117, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody

; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-117

Query Match      84.9%; Score 1592; DB 14; Length 470;
Best Local Similarity 66.6%; Pred. No. 2.4e-100;
Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
QY 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
DB 61 GQGLEWMMGEIDPSDSYTNYNQKFKGKATLTVDTTSTAYMELSLRSSEDTAVYFCARNRD 120
QY 121 MA-----YMGQGTLTAVTSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVTS 174
DB 121 YSNWNYFDVWEGTLTVTSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEP 234
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEP 240
QY 235 KSCDKHTCTCPCP----- 247
DB 241 KSCDKHTCTCPCPAPPELLGSPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
DB 361 KAKGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSFGK 354
DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSFGK 470

RESULT 14
US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
```

US-10-384-933-117

Query Match	84.9%	Score	1592;	DB	14;	Length	470;
Best Local Similarity	66.6%	Pred. No.	2.4e-100;				
Matches	313;	Conservative	17;	Mismatches	24;	Indels	116;
Gaps	2;						
QY	1	MGWSLILLFLVAVATRVLSQVQVQSGAEVVKPGASVKISKASGYVTFTHDIAHWVKQP	60				
Db	1	MGWSCILLFLVATATGVHSQVQLVQSGAEVVKPGASVKVSKASGYTFTSYWQWVKQAP	60				
QY	61	GQRLEWIGYFSPGNDPFKNYERKPKATLTADTSTASTAYVELSSLSRSEDATVFCRSLN	120				
Db	61	GQGLEWMEIDPDSYTNQKFKGKATLTVDITSTSTAYNELSSLSRSEDATVYVCARNRD	120				
QY	121	MA-----YWGQGTTLVTSSASTKGPSVFPLPSSKSTSGTGAALGCLVKDYKPPETVTS	174				
Db	121	YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLPSSKSTSGTGAALGCLVKDYKPPETVTS	180				
QY	175	WNSGALTSGVHTTTPAVLQSSGLYSLSGVTVTPSSSLGTQTYIICNVNHKPSNTKVDKKVEP	234				
Db	181	WNSGALTSGVHTTTPAVLQSSGLYSLSGVTVTPSSSLGTQTYIICNVNHKPSNTKVDKVEP	240				
QY	235	KSCDKHTHTCPPCP-----	247				
Db	241	KSCDKHTHTCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNV	300				
QY	248	-----	247				
Db	301	YVDGVEVHNAKTKPRREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI	360				
QY	248	---GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV	304				
Db	361	KAKGQPREPOVYTLPPSRDEETKNNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV	420				
QY	305	LSDSGFFFLYSKLTVDKSRWQQGNVFCSCVMYHEALNNHYTKQSLSPGK	354				
Db	421	LSDSGFFFLYSKLTVDKSRWQQGNVFCSCVMYHEALNNHYTKQSLSPGK	470				

Search completed: March 23, 2005, 18:40:00
Job time : 112.061 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1127.5	60.1	469	2	S37483	Ig gamma-2a chain C	
2	1116	59.5	330	1	GHRU	Ig gamma-1 chain C	
3	1094	58.3	446	2	S40295	Ig gamma-2b chain	
4	1066	56.8	474	1	G2S111	Ig gamma-2b chain	
5	1030.5	54.9	475	2	SWS1321	Ig gamma-2b chain	
6	1006	53.6	326	1	G2H57	Ig gamma-2 chain C	
7	997.5	53.2	377	2	A23511	Ig gamma-3 chain C	
8	995.5	53.1	377	2	A60764	Ig gamma-3 chain C	
9	981.5	52.3	444	2	PC4436	monoclonal antibody	
10	974.5	51.9	327	1	G4HU	Ig gamma-4 chain C	
11	946	50.4	470	2	S22080	Ig heavy chain pre	
12	940	50.1	472	2	S31459	Ig gamma-1 chain -	
13	852	45.4	374	2	S69339	Ig heavy chain V r	
14	814.5	43.4	241	2	S69131	Ig heavy chain (DO	
15	809	43.1	246	2	S38950	Ig gamma chain - m	
16	803.5	42.8	249	2	S69340	Ig heavy chain VH	
17	777	41.4	220	2	A94444	Ig gamma-1 heavy c	
18	769	41.0	548	2	S38864	Ig epsilon chain C	
19	748	39.9	218	2	A36040	Ig heavy chain V-1	
20	737	39.3	328	2	I47159	Ig gamma 2a chain	
21	733	39.1	328	2	I47158	Ig gamma 1 chain c	
22	732	39.0	328	2	I47161	Ig gamma 3 chain c	
23	731	39.0	328	2	I47160	Ig gamma 2b chain	
24	726	38.7	214	2	PC4202	monoclonal antibody	
25	722.5	38.5	323	1	GHRB	Ig gamma chain C r	
26	722	38.5	322	2	PS0019	Ig gamma-2a chain	
27	720	38.4	326	2	PS0017	Ig gamma-1 chain C	
28	715.5	38.1	221	2	S49220	Ig gamma-1 chain -	
29	707	37.7	549	2	S04845	Ig heavy chain pre	

	Qy	1	MGWSLILFLFVAVATRVLSQVLVQSQAEEVVKPGASVKISCKASGYTFPTDHALHWKQP	60
	Dd	1	MGWSIFLLSLLSGTAGVHCQIQQQSQPELVKPGASVKISCKASGYTFDYIYNWYKQP	60
	Qy	61	GQRLEWICYSPGNDDFKYNERKGAITADTSASTAYVELSSLSSEDTAVVFCTRSLN	120
	Dd	61	GOGLKWIGWIYPASGNTKYNEFNKGATLTVDTSSTAYNQJSSLTSETAVVFCARAMG	120
	Qy	121	-----MAYWGOGTLVTVSSASTKGPSFPPLAPSSKTSGGTAALGCLVXDYFPPEPTVS	175
	Dd	121	ATA TLIDYWGGTTLTVSSAKTTAPSVPYPLAPVGDTTGSSVTLGCLVKGYPPEPTLTW	180
	Qy	176	NSGALTGVHFTPAVLQSSGLYSLSVVTPVSSSLGTQTVCINNVHKPSNKTVDKKVEPK	235
	Dd	181	NSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSTWPSQSITCNVAHPASSTKVDKKIEPR	239
	Qy	236	SCDKTHTCPPC-----	246
	Dd	240	G-PTIKCPCCPCPAPNLGLGPSVFPPPKIKDVLMSLSPIVTCVVVDVSED DDPDVQS	298
	Qy	247	-----	246
	Dd	299	WFVNVEVHTAQOTHRDYNSTLRVVSALPIHQDMMSGKEFKCVNNKNDLPAP IERTI	358
	Qy	247	---PQPREPOVYTLPSPRDELTKNQVSLTCLVKGFVPSDIAVEWESNGPENNYKTTTP	303
	Dd	359	SKPKGSVRAPQVYVLPPEEEMTKQVTLTCMTWDWPEDIYVEWTNGKTELNYKNTEP	418
	Qy	304	VLDSDGSFFLYSKLTVDKSRWAAQGNVFSCSVMHEALHNHYTQKSLSLSPGK	354

Db 419 VLDSGYSYFMYSKLRVEKKNWVERNSYSCSVVHGLNHNHTTKSFSTPGK 469

RESULT 2

GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:CROSS-references: UNIPROT:P01857; EMBL:Z17370
A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A>Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:CROSS-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-135 <CUN>
A>Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1504, 1976
A>Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie).
igen Primärstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A>Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A>Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:6884994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A>Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A>Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:CROSS-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
C:Intron: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 59.5%; Score 1116; DB 1; Length 330;
Best Local Similarity 66.7%; Pred. No. 4.2e-60;
Matches 220; Conservative 0; Mismatches 0; Indels 110; Gaps 1;

Qy 135 ASTKGPSVFLAPSSKTSQGTAAALGCLVKDYPEPVTVSNWNSGALTSGVHTFPVAVLQSS 194
Db 1 ASTKGPSVFLAPSSKTSQGTAAALGCLVKDYPEPVTVSNWNSGALTSGVHTFPVAVLQSS 60

Qy 195 GLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKVEPKSCDKHTCTCPCP----- 247
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKVEPKSCDKHTCTCPCPAPPELLGG 120

Qy 248 ----- 247
Db 121 PSVFLFPFKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy 248 -----GQPREPQVYTLPPSRDE 264
Db 181 STYRWVSVLTVLHODWLNKYEKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240

Qy 265 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLYSKLTVDKSRW 324
Db 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLYSKLTVDKSRW 300

Qy 325 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 3
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
A:CROSS-references: UNIPROT:Q99L25
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CHR>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMH>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

P:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 58.3%; Score 1094; DB 2; Length 446;

Best Local Similarity 48.9%; Pred. No. 1.2e-58;

Matches 219; Conservative 41; Mismatches 72; Indels 116; Gaps 4;

Qy 20 QVQLVQSGAEVVKPCASVKISCKASGYTFTDHAHVKVQKQRLQLEWIGYSPRGNDPKY 79
 Db 1 QQLQSQGPELVKPCASVKISCKASGYTFTDHYIHVKVQKQRLQLEWIGYSPRGNDPKY 60
 Qy 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTR--SLNMAVWGQGTIVTVSSAST 137
 Db 61 NEKPKGKATLTDTSSSTAYVQLSSLTSEDYAVYFCARGKPFMDYWGQGTIVTVSSAKT 120
 Qy 138 KGPSVFPPLAPSKSTSGGTALGCLVKKYFPFPPVTVSNWNGALTSVGVTFPAVLQSSGLY 197
 Db 121 TAPSVYPLAPVCGDITGSSVTGLVKKYFPFPPVTVLTWNSGSLSSGVHTFPAVLQSD-LY 179
 Qy 198 SLSSVTVTPSSSLGQTQYICNVNHPKSNKVDKVEPKSCDKTHTCPPC----- 246
 Db 180 TLSSSVTVTPSSVQSSQTCNVHPASSTKVDKVEPKSCDKTHTCPPC----- 238
 Qy 247 ----- 246
 Db 239 SVFIFPKIKDVLMSLSPWTCVVVDSEDDPDVQISFVFNVNVEVLTAQTQTHREDYNS 298
 Qy 247 -----PGQPREPQVYTLPPSRDEL 265
 Db 299 TLRVVSALPIQHDWNSGKFKKVNKNDLPAPIERTISKPKSVRAQVYVLPPEEEM 358
 Qy 266 TKNQVSLCLVKGFPSPDIANWESNGQPNKYKTPPVLDSGDSFFLYSLKLVTKDSRWQ 325
 Db 359 TKQVQLTLCVMTDFMPEDYVETWVNGKTELNYKNTPEVLDSDGSYFMYSLKRVKQNV 418
 Qy 326 QGNVPSCSVMHEALNHNHYTKSLSPG 353
 Db 419 ERNSVCSVNVHGLNHNHYTKSPRTG 446

RESULT 4

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004

C:Accession: S25057; A02157; A26235; A26232; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m

A:Reference number: S25057

A:Accession: S25057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: UNIPROT:P01866; EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.

Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m

A:Reference number: A02157; MUID:80120716; PMID:6766534

A:Contents: a allele

A:Accession: A02157

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>

A:Cross-references: GB:J00461

A>Note: the sequence was determined from the germline gene

R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea

A:Reference number: A26235; MUID:80081501; PMID:117548

A:Contents: MPC 11

A:Accession: A26235

A:Molecule type: mRNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>

A>Note: Lys-474 is probably removed posttranslationally

R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.

Science 206, 1303-1306, 1979

A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob

A:Reference number: A26232; MUID:80081502; PMID:117549

A:Accession: A26232

A:Molecule type: DNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>

R:Ollo, R.; Rougeon, F.

Nature 296, 761-763, 1982

A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gam

A:Reference number: A26233; MUID:82173203; PMID:6803173

A:Contents: b allele

A:Accession: A26233

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLI>

A:Cross-references: GB:J00461

R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Mateunaga, C.; Yamamoto, K.; Izimura, T.; Takahash

J. Biol. Chem. 269, 12345-12350, 1994

A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A:Reference number: A53598; MUID:94216359; PMID:7512967

A:Accession: A53598

A>Status: preliminary

A:Molecule type: protein

A:Residues: 234-251 <KIM>

C:Comment: The a allele sequence is shown.

C:Genetics:

A:Introns: 138/1; 236/1; 258/1; 368/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaf

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob

F:157-222/Domain: immunoglobulin homology <IM1>

F:236-257/Region: hinge

F:281-350/Domain: immunoglobulin homology <IM2>

F:387-454/Domain: immunoglobulin homology <IM3>

F:152/Disulfide bonds: interchain (to light chain) #status predicted

F:164-220,288-348,394-452/Disulfide bonds: #status predicted

F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted

F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.8%; Score 1066; DB 1; Length 474;

Best Local Similarity 45.6%; Pred. No. 6.1e-57;

Matches 216; Conservative 49; Mismatches 89; Indels 120; Gaps 4;

Qy 1 MGWLLILFLVAVTRVLSQVLVQSGAEVVKPCASVKISCKASGYTFTDHAHVKVQKMP 60
 Db 1 MEWSWIFLLSLGAGVHSEVQLQSGPELVNPGASVKISCKASGYTFTTYVHVWVKQKP 60
 Qy 61 GQRLWIGYFSPGNDDFKYNRFGKATLTADTSASTAYVELSLRSEDYAVYFCTSLN 120
 Db 61 QQGLEWIGYINPNKDGTFKNEKFKATLTSDKSNATYMELSLTSDSAVYVCARDYD 120
 Qy 121 ---MAYWQGTIVTVSSASTKPSVFPPLAPSKSTSGGTALGCLVKKYFPFPPVTVSNWS 177
 Db 121 YDNFAYWQGTIVTVSSAKTTPPSVYPLAPCGDITGSSVTSGCLVKGFFPESVTVTWS 180
 Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSNKVDKVEPKSKS- 236
 Db 181 GSLSSVHTLSQALLQSGLYTMSSSVTVTPSSVTPSQVTCVSAHPASSTVTDVKLEPSPG 240
 Qy 237 -----CDKTHTCP----- 244

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Db      241  ISTINPCPCKECHKCPAPNLEGGSPVFIFPPNIKDVLMISLTPKVTCTVVVDVSEDDPDV 300
QY      245  -----PCP-- 247
Db      301  QISFVNNVVEHTAQOTQTHREDYNSTIRVSTLPIQHQDWSGKEFKCKVNNKOLPSPIE 360
QY      248  -----QOPREPQVYTLPPSRDELTKNQSVLCLVKGFPYSDIAVEVSNQGPENNYKT 300
Db      361  RTISKIKGLVRAPOVYILPPPAEQLSRKDVSLTCLVGVFNPCDISVETWSNGTTEENYKD 420
QY      301  TPPVLDSGSGFLYSKLVTDKSRWQGNVFCGSVMHEALHNYTKSLSPGK 354
Db      421  TAPVLDSGSGFYISKLNKMTSKMEKTDSCFNVRHEGLKNYLTKTISRSPGK 474

RESULT 5
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Piers, W.
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DEL>
A:CROSS-references: EMBL:X13188; NID:g51780; PID:CAA31580.1; PID:g51781
A:Note: This sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <WAT>
F:159-233/Domain: immunoglobulin homology <IMM>

Query Match      54.9%; Score 1030.5; DB 2; Length 475;
Best Local Similarity 45.0%; Pred. No. 8.3e-55;
Matches 214; Conservative 47; Mismatches 99; Indels 123; Gaps 5;

QY      1  MGWSLILFLVAVTRVLVSQVLQSGAEVVKPGASVKISKASGYFTDHAHHVKQNP 60
Db      1  MEWIFILSILGTAGVQSGVQLQSGAEVVKPGASVKISKASGYFTDHAHHVKQNP 60
QY      61  GQRLWIGYFPGNDDFKYNRFKGAATLADTASTAYVELSLRSDTAVYFCTRS-- 118
Db      61  GQGLEWIGEYFPGNSVFNKFKGKATLVDKSSSTAYLHLSLTSSEDSAVYFCAGPRQ 120
QY      119  ---LNMAYWGQGLTVTVSSASTKGPSVPLAPSKSTSGGTAALGCLVKDYFPEPTVSW 175
Db      121  VGLLPFGYWGQGLTVTASAAKTPPSVYPLAPGCGDTTGSSTGLCLVKGYFPEPTVW 180
QY      176  NSGALTSGVTHFPAVLQSGGYSLSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPK 235
Db      181  NSGSLSSVSHFTFPALLQ--SGLYTWSSTVTPSPSTWPTVTCVAHPASSTVDKLEPS 239
QY      236  S-----CDKTHTCP----- 244
Db      240  GPTSTINPCPCKECHKCPAPNLEGGSPVFIFPPNIKDVLMISLTPKVTCTVVVDVSEDDP 299
QY      245  -----PCP 247
Db      300  DVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHQDWSGKEFKCKVNNKOLPAP 359
QY      248  -----QOPREPQVYTLPPSRDELTKNQSVLCLVKGFPYSDIAVEVSNQGPENNY 298
Db      360  IERTISKIKGLVRAPOVYILPPPAEQLSRKDVSLTCLVGVFNPCDISVETWSNGTTEENY 419
QY      299  KTTTPVLDSGSGFLYSKLVTDKSRWQGNVFCGSVMHEALHNYTKSLSPGK 354
Db      420  KDTAPVLDSGSGFYISKLNKMTSKMEKTDSCFNVRHEGLKNYLTKTISRSPGK 475

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RESULT 6

G2HU

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Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:CROSS-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Conneil, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOP>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:CROSS-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbonyl group (Asn) (covalent) #status predicted

```

```
Query Match      53.6%; Score 1006; DB 1; Length 326;
Best Local Similarity 61.1%; Pred. No. 1.6e-53;
Matches 201; Conservative 7; Mismatches 9; Indels 112; Gaps 2;

QY 135 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60

QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCP 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVKRCVBE---CPPCPAPPVAGP 117

QY 248 ----- 247

DB 118 SVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVFNHNAKTKPREEQNS 177

QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVK 265
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 178 TFRVSVLTVVHQDNLGKEYKCKVSKNGLPAPIEKTISTKYGQPREPQVYTLPPSRDEM 237

QY 266 TKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRMQ 325
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 238 TKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRMQ 297

QY 326 QGNVPSCSMHEALHNHYTQKSLSLSPGK 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 298 QGNVPSCSMHEALHNHYTQKSLSLSPGK 326

RESULT 7
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match      53.2%; Score 997.5; DB 2; Length 377;
Best Local Similarity 53.8%; Pred. No. 6.2e-53;
Matches 203; Conservative 8; Mismatches 9; Indels 157; Gaps 2;

QY 135 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60

QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVV----- 232
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GLYSLSSVTVTPSSSLGTQTYTCNVNHNKPSNTKVDKRVELKTLPLGDTTHTCPCPEPKSC 120

QY 233 -----EPKSCDKTHTCPPCP----- 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTP 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVFNHNAKTKPREEQNSTFRVSVLTVLH 240

QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVK 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 QDWLNGKEYKCKVSKNKAAPLAPIEKTISTKYGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300

QY 278 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 337
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 ALHNRYTQKSLSLSPGK 377

RESULT 9
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
```

```
QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVK 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 QDWLNGKEYKCKVSKNKAAPLAPIEKTISTKYGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300

QY 278 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 337
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 ALHNRYTQKSLSLSPGK 377

RESULT 8
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match      53.1%; Score 995.5; DB 2; Length 377;
Best Local Similarity 53.8%; Pred. No. 8.2e-53;
Matches 203; Conservative 8; Mismatches 9; Indels 157; Gaps 2;

QY 135 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSS 60

QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVV----- 232
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 GLYSLSSVTVTPSSSLGTQTYTCNVNHNKPSNTKVDKRVELKTLPLGDTTHTCPCPEPKSC 120

QY 233 -----EPKSCDKTHTCPPCP----- 247
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTP 180

QY 248 ----- 247

DB 181 LMISRTPEVTCVVVDVSHEDPEVFQFNWYDGVFNHNAKTKPREEQNSTFRVSVLTVLH 240

QY 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVK 277
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 QDWLNGKEYKCKVSKNKAAPLAPIEKTISTKYGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300

QY 278 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 337
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKSRWQGNVFSCVMHE 360

QY 338 ALHNHYTQKSLSLSPGK 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 ALHNRYTQKSLSLSPGK 377

RESULT 9
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
```

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A;Reference number: JCS810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase activity. It is directed against hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 52.3%; Score 981.5; DB 2; Length 444;
Best Local Similarity 41.9%; Pred. No. 6.7e-52;
Matches 188; Conservative 66; Mismatches 76; Indels 119; Gaps 5;

QY 20 QVQLVQSGAEVVKPKASVKISCKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDF-- 77
DB 1 EQVQVETGGGLVPGNSKLSCLTSGFTFSNHWLQPPKRLWIAVITVKSNDYGA 60

QY 78 KYNERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRS---LNMYWGQGLTVTVSS 134
DB 61 KYAESVRGRFTISRDDSKSSVYLQNNRLREEDTATYYCCRTPWVYAMDCWGQTSVIYSS 120

QY 135 ASTKGPSVFPPLAPSKSTSGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPVAVLOSS 194
DB 121 AKTTPPSVYPLAPGSAATQNSMVTILGCLVKGYFPEPTVTVSNWNSGSLSGVHTFPVAVLOSS 180

QY 195 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPC----- 246
DB 181 -LYTLSSSVTVTPSSWTPSETVTCNVHPASSTKVDKLVPRDCG----CKPCICTVPEVS 235

QY 247 ----- 246

DB 236 SVFIFPPKPKDVLITITLTKPVTVVVDISKDPEVQSFVDFVDDVEVHTAQTQPREEQENS 295

QY 247 -----PGPREPQVTLPPSRDEL 265

DB 296 TFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEKTIKTKGRPKAPQVYTIPTPPKEQM 355

QY 266 TKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQ 325
DB 356 AKDKVSLTCMTIDFPEDITVEWQNGQPAENYKNTQFIMTDGSGFYISKLVNPKSNWE 415

QY 326 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 416 AGNTFTCSVLHLEGLHNHTKLSLSHPGK 444

RESULT 10
G4HU
I; gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: The sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14Q32.33-14Q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 974.5; DB 1; Length 327;
Best Local Similarity 59.7%; Pred. No. 1.3e-51;
Matches 197; Conservative 9; Mismatches 11; Indels 113; Gaps 2;

QY 135 ASTKGPSVFPPLAPSKSTSGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPVAVLOSS 194
DB 1 ASTKGPSVFPPLAPSKSTSGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPVAVLOSS 60

QY 195 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPC----- 247
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPC----- 117

QY 248 ----- 247

DB 118 PSVFLFPPKPKDVLITITLTKPVTVVVDVSDQDEPEVQFNWYVDGVEVHNKTKPREEQFN 177

QY 248 -----GQPREPQVTLPPSRDE 264

DB 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTIPTPPQEE 237

QY 265 LTRNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 324
DB 238 MTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 297

QY 325 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 298 QEGNVFCSCVMHEALHNHYTQKSLSLSPGK 327

RESULT 11
S22080
I; heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 50.4%; Score 946; DB 2; Length 470;
Best Local Similarity 42.2%; Pred. No. 9.7e-50;
Matches 201; Conservative 51; Mismatches 90; Indels 134; Gaps 10;

QY 3 WSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
DB 5 WT--LLFVLSAPIGVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
QY 63 RLEWIGYSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDVAVFYCTRLNNA 122
DB 63 ALEWVGITSGTIV--YNPALKSRLSITKENSQVLSVSVTPEDTATYCAR--T 118
QY 123 Y-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAAAGCLVKDYFPP 171
DB 119 YGEVGDGAIDAWGQGLLTVSSASTAPKVVYPLSSCCGDKSSSVTLGLCLVSSYMP 178
QY 172 TVSNHGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDK 231
DB 179 TVTNHGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDK 237
QY 232 VE-----PKSCDKHTHTCP--CPGP----- 250
DB 238 VDPTCKPSPCD---CCPPELPGSPVFIFFPKPKDITLTISGTPEVTCVVVDVGHDDPEV 294
QY 251 ----- 250
DB 295 KFSFVDDVEVNTATKPREEQFNSTYRVVSALRIHQDWTGKGEKFKCKVHNEGLPAPIV 354
QY 251 -----REPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOP--ENNY 298
DB 355 RTISTKGPAREPQVYVLAAPPQELSKSTVLTCTMTVTFYFDYIAVEWQNGQPESEDKY 414
QY 299 KTTPLVDSGDFLYSKLTVDKSRWQGNVFCVSVHAEALHNHYTKSLSPK 354
DB 415 GTTPQLDADSGYFLYSLRLVDRNSWQEGDYIACVHAEALHNHYTKSLSPK 470

RESULT 12
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A:Reference number: S31459
A:Accession: S31459
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <PAT>
A:Cross-references: EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 50.1%; Score 940; DB 2; Length 472;
Best Local Similarity 41.9%; Pred. No. 2.2e-49;
Matches 198; Conservative 56; Mismatches 95; Indels 124; Gaps 7;

QY 3 WSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
DB 3 WT--LLFVLSAPRGVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 60
QY 63 RLEWIGYSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDVAVFYCTR----- 117
DB 61 ALEWLG--GSGYDEDIDYNPVLSRSLITKTSKQVSLTSTVTEDTAVYCARVDYS 119
QY 118 SLNWAY-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAAAGCLVKDYFPP 172
DB 120 SHAFAYASYDFWFGPLLISVLSASTTPPKVPLTSCCGDTSSIVTLGLVSSYMPPEPT 179

Query Match 45.4%; Score 852; DB 2; Length 374;
Best Local Similarity 48.8%; Pred. No. 3.3e-44;
Matches 185; Conservative 44; Mismatches 106; Indels 44; Gaps 9;

QY 8 LFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTH--AIHWKQNPQORLE 65
DB 8 LLLLTIPSWSLVSQITLKESGPTLVKPTQTLTCTFGSLSKSGVGVWIRPQGOALE 67
QY 66 WIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDVAVFYCTRSL---NWA 122
DB 68 WLALIF--WDDDKRYSPSLRTRLTITKDTSKNQVLTMTNVDPADTATYCGYSVEG 126
QY 123 Y-----WGQGLTVTVSSASTK-----GPSVFPLAPSSKST--SGTAAAL 159
DB 127 YRFHSWGQGLTVTVSSSEPKSCDKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEV 186
QY 160 GCLVKDYFPPPEVTVSN---SGALTSGVHTFPVAVLQSSGLYSLSVTVVPSST--LGTQTY 215
DB 187 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEY 246
QY 216 ICNVNHPKSNTKVDKVEPKSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCL 275
DB 247 KCVSNKALPAPIEK-----TISKAGQPREPQVYTLPPSRDELTKNQVSLTCL 295
QY 276 VKGYFVPSDIAVEWESNGOPENNYKTTPLVDSGDFLYSKLTVDKSRWQGNVFCVSVH 335

RESULT 13
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of a normal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KGA>
A:Cross-references: EMBL:X81695
R:Khamilichi, A.A.
Submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 45.4%; Score 852; DB 2; Length 374;
Best Local Similarity 48.8%; Pred. No. 3.3e-44;
Matches 185; Conservative 44; Mismatches 106; Indels 44; Gaps 9;

QY 8 LFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTH--AIHWKQNPQORLE 65
DB 8 LLLLTIPSWSLVSQITLKESGPTLVKPTQTLTCTFGSLSKSGVGVWIRPQGOALE 67
QY 66 WIGYFSPGNDPKYNERFKGKATLTADTSASTAYVELSLRSEDVAVFYCTRSL---NWA 122
DB 68 WLALIF--WDDDKRYSPSLRTRLTITKDTSKNQVLTMTNVDPADTATYCGYSVEG 126
QY 123 Y-----WGQGLTVTVSSASTK-----GPSVFPLAPSSKST--SGTAAAL 159
DB 127 YRFHSWGQGLTVTVSSSEPKSCDKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEV 186
QY 160 GCLVKDYFPPPEVTVSN---SGALTSGVHTFPVAVLQSSGLYSLSVTVVPSST--LGTQTY 215
DB 187 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEY 246
QY 216 ICNVNHPKSNTKVDKVEPKSCDKHTCTCPGCPGPREPQVYTLPPSRDELTKNQVSLTCL 275
DB 247 KCVSNKALPAPIEK-----TISKAGQPREPQVYTLPPSRDELTKNQVSLTCL 295
QY 276 VKGYFVPSDIAVEWESNGOPENNYKTTPLVDSGDFLYSKLTVDKSRWQGNVFCVSVH 335

```

Db      296 VKGFVPSDIATWESNGQPNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVPSCSVM 355
Qy      336 HEALHNHYTKQSLSPGK 354
      |||||
Db      356 HEALHNHYTKQSLSPGK 374
      |||||

RESULT 14
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin Igg Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; MUID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <WAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      43.4%; Score 814.5; DB 2; Length 241;
Best Local Similarity 66.8%; Pred. No. 3.7e-42;
Matches 163; Conservative 23; Mismatches 47; Indels 11; Gaps 4;

Qy      20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNPQORLEWIGYFSPGNDDPKY 79
      |||||
Db      1 QIQLQSQGPVLVPGASVKISKASGYTFTDYYIHVKQRPGEGLWIGWIYPGSGNTKY 60
      |||||

Qy      80 NERFKGKATLTADTSASTAYVELSLRSEDNAVYFCTR---SLNWAYWGQGLVTPAVLQSSGLY 197
      |||||
Db      61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYMGQGTSTVTSSAKT 120
      |||||

Qy      138 KGPSVFPPLAPSSKTSSTGTAALGCLVKDYPPPTVSWNSGALTSGVHTTTPAVLQSSGLY 197
      |||||
Db      121 TAPSVIPLAPVCGDTTSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTTTPAVLQSSD-LY 179
      |||||

Qy      198 SLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCTCPPC-----PQQPREP 253
      |||||
Db      180 TLSSSVVTSTWSPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGP 238
      |||||

Qy      254 QVYTLPP 260
      |||
Db      239 SVFIIPP 245
      |||

Search completed: March 23, 2005, 18:36:51
Job time : 35.7778 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:05:41 ; Search time 136.475 Seconds
(without alignment)
1328.275 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGRSLILLFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1521.5	81.1	469	Q7Z7P5	Q7Z7P5 homo sapien
2	1500.5	80.0	475	Q6N095	Q6N095 homo sapien
3	1479	78.8	480	Q6PJF1	Q6PJF1 homo sapien
4	1440	76.8	472	Q6N089	Q6N089 homo sapien
5	1439	76.7	518	Q6N030	Q6N030 homo sapien
6	1430.5	76.3	475	Q6MZQ6	Q6MZQ6 homo sapien
7	1427.5	76.1	544	Q6PJ95	Q6PJ95 homo sapien
8	1426	76.0	466	Q6IN78	Q6IN78 homo sapien
9	1425	76.0	470	Q6PJ44	Q6PJ44 homo sapien
10	1422.5	75.8	475	Q6GMW7	Q6GMW7 homo sapien
11	1417	75.5	466	Q6N096	Q6N096 homo sapien
12	1410	75.2	478	Q6PI81	Q6PI81 homo sapien
13	1407.5	75.0	473	Q6MZV7	Q6MZV7 homo sapien
14	1402	74.7	480	Q6N094	Q6N094 homo sapien
15	1400	74.6	482	Q7Z351	Q7Z351 homo sapien
16	1398.5	74.5	473	Q6P055	Q6P055 homo sapien
17	1392	74.2	470	Q7Z5W1	Q7Z5W1 homo sapien
18	1379.5	73.5	465	Q6GMX6	Q6GMX6 homo sapien
19	1377.5	73.4	481	Q6N097	Q6N097 homo sapien
20	1374	73.2	476	Q6GMX1	Q6GMX1 homo sapien
21	1330	70.9	464	Q6MZU6	Q6MZU6 homo sapien
22	1322	70.5	493	Q68CN4	Q68CN4 homo sapien
23	1285.5	68.5	465	Q6P6C4	Q6P6C4 homo sapien
24	1284.5	68.5	521	Q8N4Y9	Q8N4Y9 homo sapien
25	1218	64.9	417	Q6N093	Q6N093 homo sapien
26	1205	64.2	473	Q8TC63	Q8TC63 homo sapien
27	1195.5	63.7	476	Q6GMZ7	Q6GMZ7 homo sapien
28	1162	61.9	348	Q6PYX1	Q6PYX1 homo sapien
29	1148.5	61.2	465	Q6PJB2	Q6PJB2 mus musculus
30	1138.5	60.7	473	Q9DBL4	Q9DBL4 mus musculus
31	1121.5	59.8	463	Q99LC4	Q99LC4 mus musculus

Query Match

81.1%; Score 1521.5; DB 2; Length 469;

ALIGNMENTS

RESULT 1

ID	Q7Z7P5	PRELIMINARY;	PRT;	469 AA.
AC	Q7Z7P5;			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	IGHG1 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUS=Spleen;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
[2]				
RW	SEQUENCE FROM N.A.			
RC	TISSUS=Spleen;			
RA	Strausberg R.;			
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC051328; AAHS1328.1; -			
DR	HSSP; P01857; 1HZH.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; CI-set; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 4.			
DR	PROSITE; PS00290; IG MHC; UNKNOWN 2.			
SQ	SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAAF795C CRC64;			

Query Match

81.1%; Score 1521.5; DB 2; Length 469;

RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.8%; Score 1440; DB 2; Length 472;
Best Local Similarity 59.3%; Pred. No. 1.le-94;
Matches 280; Conservative 33; Mismatches 41; Indels 118; Gaps 2;

QY 1 MGWLSILLFLVAVATRVLSQVQVSGAEVVKPGASVKISKASGYTFTDHAHHVKNP 60
DB 1 MDWTRFLFVVAATGVQSQVQVSGAEVVKPGASVKISKASGGSGFVSWRQAP 60

QY 61 GQRLWIGYFSGNDDFKYNERFKGKATLTADTSASTAYVELSLRSSEDTAVYFCTSL- 119
DB 61 GQGLAWGGIIPAFDITKYAQNFQDRVTISADESDTAYMELSLRSSEDTATYYCARDLA 120

QY 120 -----NMAYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLV 172
DB 121 LYELWSGFHTDEKYYGLDVGWGGTPTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLV 180

QY 165 DYFPEPTVTVSSNGALTSGVHTFPAVLQSSGLYSLSVTVVPSSSLGQTQYICNVNHRKPS 224
DB 181 DYFPEPTVTVSSNGALTSGVHTFPAVLQSSGLYSLSVTVVPSSSLGQTQYICNVNHRKPS 240

QY 225 NTKVDKKEPKSCDKTHTCPPCP----- 247
DB 241 NTKVDKKEPKSCDKTHTCPPCPAPELGPGSVFLPPPKPDTLMISRTPEVTCVVVDVS 300

QY 248 ----- 247
DB 301 HEDPEVKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 360

QY 248 -----GOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 294
DB 361 LPAPLEKTIISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 420

QY 295 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 354
DB 421 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 480

RESULT 4
Q6N089
ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686p15220.
GN Name=DKFZp686p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;

RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.8%; Score 1440; DB 2; Length 472;
Best Local Similarity 59.3%; Pred. No. 1.le-94;
Matches 280; Conservative 33; Mismatches 41; Indels 118; Gaps 2;

QY 1 MGWLSILLFLVAVATRVLSQVQVSGAEVVKPGASVKISKASGYTFTDHAHHVKNP 60
DB 1 MELGTWTFLLAILKGVQCEVQLVESGGGLVQPGKSLRLSCAASGFTFDDYAMHWVRQAP 60

QY 61 GQRLWIGYFSGNDDFKYNERFKGKATLTADTSASTAYVELSLRSSEDTAVYFCTSL- 119
DB 61 GQGLWWSGSIWNSGSIAYADSVKGRFTISRDNKNSLYLQWNSLRAREDYLYCAKEIG 120

QY 120 -----NMAYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLV 172
DB 121 AHNFYTYGMDVWGGTPTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLV 180

QY 173 VSWNSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSSLGQTQYICNVNHRKPSNTKVDKV 232
DB 181 VSWNSGALTSGVHTFPAVLQSSGLYSLSVTVVPSSSLGQTQYICNVNHRKPSNTKVDKV 240

QY 233 EPKSCDKTHTCPPCP----- 247
DB 241 EPKSCDKTHTCPPCPAPELGPGSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKF 300

QY 248 ----- 247
DB 301 NWYVDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 360

QY 248 -----GOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 302
DB 361 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 420

QY 303 PVLDSGDSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 354
DB 421 PVLDSGDSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 472

RESULT 5
Q6N030
ID Q6N030 PRELIMINARY; PRT; 518 AA.
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686p115212.
GN Name=DKFZp686p115212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;

RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; -;
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 76.7%; Score 1439; DB 2; Length 518;
Best Local Similarity 55.6%; Pred. No. 1.5e-94;
Matches 288; Conservative 28; Mismatches 38; Indels 164; Gaps 3;

QY 1 MGSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNP 60
DB 1 MDWTRILFLVTAIGAHSQVHLVQSGAEVVKPGASVKISCTASGYFTFTDHAHHVKQNP 60

QY 61 GQRLWIGYFPGNDDFKYNRPKATLTADTSASTAYVELSLRSDEDTAVYFCTRSLN 120
DB 61 GQSLWGMWINTGNKTKYKQFGQRTITRDITTTAYMDLSLSRSEDATVAVYWCARDAP 120

QY 121 MA-----YQGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTV 173
DB 121 QGVTTTTFDYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTV 180

QY 174 SWNSGALTSVHTTTPAVLQSSGLYSLSSVTVPSSSLGTTQYICNVNHPKNTKVDKKV- 232
DB 181 SWNSGALTSVHTTTPAVLQSSGLYSLSSVTVPSSSLGTTQYICNVNHPKNTKVDKRV 240

QY 233 -----EPKSCDKTHTCPPC 246
DB 241 LKTPLDGTTHTPCRPCKPCDTPPCPCPEKSCDTPPCPCPEKSCDTPPCPCRC 300

QY 247 P----- 247
DB 301 PAPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKT 360

QY 248 -----GQPREPOVY 256
DB 361 KPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKTKGQPREPOVY 420

QY 257 TLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 316
DB 421 TLPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPPMLDSGSGFFLYSK 480

QY 317 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 481 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 518

RESULT 6

Q6MZQ6
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp6866G11190.
GN Name=DKFZp6866G11190;
OS Homo sapiens (Human).

RESULT 7

Q6PJ95
ID Q6PJ95 PRELIMINARY; PRT; 544 AA.
AC Q6PJ95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -;
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 76.3%; Score 1430.5; DB 2; Length 475;
Best Local Similarity 59.2%; Pred. No. 5.3e-94;
Matches 281; Conservative 36; Mismatches 37; Indels 121; Gaps 3;

QY 1 MGSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNP 60
DB 1 MEFLGLWFLVAILKGQCEVQLLESGLGVQPGSLRLSCAASGFTFRYAMNVRQAP 60

QY 61 GQRLWIGYFPGNDDFKYNRPKATLTADTSASTAYVELSLRSDEDTAVYFCTRS-- 118
DB 61 GKGLEWYSGISSGGVNTYADSVKGRFTISGDISTNTLYLQMHSLRADDATVAVYCARADY 120

QY 119 -----LNMA-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPE 169
DB 121 RDQVSPAYVYFDVWGRGTLVSVSAASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPE 180

QY 170 PVTVMNSGALTSGVHTTTPAVLQSSGLYSLSSVTVPSSSLGTTQYICNVNHPKNTKVD 229
DB 181 PVTVMNSGALTSGVHTTTPAVLQSSGLYSLSSVTVPSSSLGTTQYICNVNHPKNTKVD 240

QY 230 KKVPEKSCDKTHTCPPC----- 247
DB 241 KKVPEKSCDKTHTCPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300

QY 248 ----- 247
DB 301 VKFNWYDGVGVHNAKTKPREEQYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360

QY 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 299
DB 361 EKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 420

QY 300 TTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
DB 421 TTPVLDSDGSGFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475


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Db 1 MEFWLSWFLVAILKGVQCEVLVSGGLIQPGGSLTSCAASGLTVSSNMEHWVRQAP 60
Qy 61 GORLEWIGVSPGNDDEFKYNREFKATLTADTASTAYVELLSRSEDYAVYFCTRS-- 118
Db 61 GKGLEWVSUVLIGGATY-YADVSGKGRFTISRDNKNTLYLQWNSLRABEDYAVYCARQNY 119
Qy 119 -LNMAWQGGTLVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTWSNS 177
Db 120 VVPAAPWQGGTLVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTWSNS 179
Qy 178 GALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVPKSC 237
Db 180 GALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVPKSC 239
Qy 238 DKTHTCPPCP----- 247
Db 240 DKTHTCPPCPAPPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 299
Qy 248 ----- 247
Db 300 GVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAK 359
Qy 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 307
Db 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 419
Qy 308 DGSFPLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 354
Db 420 DGSFPLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 466

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RESULT 9

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Q6FJA4
ID Q6FJA4 PRELIMINARY; PRT; 470 AA.
AC Q6FJA4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 76.0%; Score 1425; DB 2; Length 470;
Best Local Similarity 59.6%; Pred. No. 1.3e-93;
Matches 280; Conservative 31; Mismatches 43; Indels 116; Gaps 2;

Qy 1 MGWSLILLLFVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHMKNP 60
Db 1 MELGLSWFLVAILLEGVQCEVLVSGGLVQPGSLRLSCVSGFTFSSTVMSWVRQAP 60
Qy 61 GORLEWIGVSPGNDDEFKYNREFKATLTADTASTAYVELLSRSEDYAVYFCTRS 120
Db 61 GKGLEWVANIKQDGEKYYVDSVKGRFTISRDNKNSLYLQWNSLRABEDYAVYCARDGS 120
Qy 121 MAY-----WGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVS 174
Db 121 SWYRDWDFPMGQGTLLTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVS 180
Qy 175 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVKPEP 234
Db 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVKPEP 240
Qy 235 KSCDKTHTCPPCP----- 247
Db 241 KSCDKTHTCPPCPAPPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYCKVSNKALPAPIEKTIS 360
Qy 248 --GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Qy 305 LDSGSPFLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 470

RESULT 10
Q6GMW7
ID Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., S.W.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krywinski M.I., Skalska J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FES5D736960F8 CRC64;

Query Match 75.8%; Score 1422.5; DB 2; Length 475;
Best Local Similarity 59.6%; Pred. No. 2e-93;
Matches 283; Conservative 28; Mismatches 43; Indels 121; Gaps 3;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHHVKQNP 60
Db 1 MEFLGSCVFLVAILFKGHCVEQLVESGGGLVQPGGSLRLSCVASFATLSRHHMHWVQAP 60

Qy 61 GORLEWIGYFPGNDDFKYNRFKQKATLTADTASATAYVELSLRSRSDTAVYFCSTRS- 118
Db 61 KGLEYVSGISSENSSTYADSVKGRFTISRDNKNTLYLQGLSLRAEDKAVYICARARC 120

Qy 119 -----LNMA-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPPE 169
Db 121 RGDTCNLFYGLDVMGQGTTVIVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPPE 180

Qy 170 PVTVSWNSGALTSVGHVTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVD 229
Db 181 PVTVSWNSGALTSVGHVTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVD 240

Qy 230 KKVEPKSCDKTHTCPCPCP----- 247
Db 241 KKVEPKSCDKTHTCPCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300

Qy 248 ----- 247
Db 301 VKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360

Qy 248 -----GPRPEQVYTLPPSRDELTKNQVSLTCLVKGYFDPDIAVWESNGQPENNYK 299
Db 361 EKTISKAKGPRPEQVYTLPPSRDELTKNQVSLTCLVKGYFDPDIAVWESNGQPENNYK 420

Qy 300 TTPPVLDSDGFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYHTOKSLSLSPGK 354
Db 421 TTPPVLDSDGFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYHTOKSLSLSPGK 475

RESULT 11
Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686i115196.
GN Name=DKF2p686i115196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RA The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1; -;
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 75.5%; Score 1417; DB 2; Length 466;
Best Local Similarity 60.3%; Pred. No. 4.8e-93;
Matches 281; Conservative 28; Mismatches 45; Indels 112; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHHVKQNP 60
Db 1 MEFLGSCVFLVAILFKGHCVEQLVESGGGLVQPGGSLRLSCVASFATLSRHHMHWVQAP 60

Qy 61 GORLEWIGYFPGNDDFKYNRFKQKATLTADTASATAYVELSLRSRSDTAVYFCSTRS- 118
Db 61 KGLEYVSLMRDDASETAYAEFVQGRFTISRDNKNTLYLQGLSLRAEDTAVYICARGGF 120

Qy 119 LNMAWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPVTVMNSG 178
Db 121 GNPDWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPVTVMNSG 180

Qy 179 ALTSVGHVTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCD 238
Db 181 ALTSVGHVTPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCD 240

Qy 239 KTHTCPCPCP----- 247
Db 241 KTHTCPCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 300

Qy 248 -----G 248
Db 301 VEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCRVSNKALPAPIEKTISKAKG 360

Qy 249 QPRPEQVYTLPPSRDELTKNQVSLTCLVKGYFDPDIAVWESNGQPENNYKTTTPVLDS 308
Db 361 QPRPEQVYTLPPSRDELTKNQVSLTCLVKGYFDPDIAVWESNGQPENNYKTTTPVLDS 420

Qy 309 GSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYHTOKSLSLSPGK 354
Db 421 GSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYHTOKSLSLSPGK 466

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RESULT 12
Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 1.
DR SMART; SM00406; IG; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 75.2%; Score 1410; DB 2; Length 478;
Best Local Similarity 57.7%; Pred. No. 1.6e-92;
Matches 276; Conservative 34; Mismatches 44; Indels 124; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVQLVQSGAEVYVVGKASVKISKASGYTFTDHAHWKQNP 60
Db 1 MELGLSWFLVAILEGVQCEIQLVQSGGLVQPGSLRLSCAASGFTFSYVMSWVRQAP 60

Qy 61 GQLEWIGYSPGNDDFKYNRFKPKATLTADTSASTAYVELSLRSDTAVYCTSLN 120
Db 61 GKGLEWVNIQDGEKTYVDVSVKGRFTISRDNAKNSLYLQMSLRADDTAVYCARFE 120

Qy 121 -----MAYWGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDY 166
Db 121 STMTVTVNADYFYFMDVWGKGTITVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDY 180

RESULT 13
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 1.
DR SMART; SM00406; IG; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BF447 CRC64;

Query Match 75.0%; Score 1407.5; DB 2; Length 473;
Best Local Similarity 57.9%; Pred. No. 2.3e-92;
Matches 274; Conservative 36; Mismatches 44; Indels 119; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVQLVQSGAEVYVVGKASVKISKASGYTFTDHAHWKQNP 60
Db 1 MELGLCWFLVAILEGVQCEIQLVQSGGLVQPGSLRLSCAASGFTFSFPMWVRQAP 60

Qy 61 GQLEWIGYSPGNDDFKYNRFKPKATLTADTSASTAYVELSLRSDTAVYCTSLN 120
Db 61 GKGLEWLSYTRSGNTVYVYADSLQGRFTISRDNARNSLYLQMSLRADDTAVYCARQNE 120

Qy 121 -----MAYWGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDY 171
Db 121 HTSPWYSPFDYWGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDY 180

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Query Match	74.6%	Score 1400;	DB 2;	Length 482;
Best Local Similarity	57.3%;	Pred. No. 8.2e-92;		
Matches	276;	Conservative	32;	Mismatches 46;
			Indels	128;
			Gaps	2
Qy	1	MGWSLILFLVAVATRVLSQVQSVQSGAEVVKPCASVKISCKASGYTFTDTHAIHWKNP	60	
Db	1	MEFGLTWFFVALRGVQCAQVVSQSGSVVQGRSURLSCIASGFFSGSAMWLRIP	60	
Qy	61	GORLEIGYFSPGNDDPKYNERFKGKATLTADTASATYVELSSLRSBEDTAYVFCSTRSLN	120	
Db	61	GKGLEWAVISYDGNHKLYSDSVKGRFTIQRDNSKSLFLFHVNSLTSADTAIYYCARDFH	120	
Qy	121	-----MAYWGOTLTAVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCL	162	
Db	121	SKTTSIFGLIPLFYYSAMDWGRGTTVIYSSASTKGPSVFPPLAPSSKTSGGTAALGCL	180	
Qy	163	VKDYPPEPVTVSNWSGALTSGVHTFFPAVLQSSGLYLSSSVTVFPSSSLGTQTYICNVNHK	222	
Db	181	VKDYPPEPVTVSNWSGALTSGVHTFFPAVLQSSGLYLSSSVTVFPSSSLGTQTYICNVNHK	240	

Qy	223	PSNTKVDKKVEPKSCDKTHTCPPCF-----	247
Db	241	PSNTKVDKKVEPKSCDKTHTCPPCFAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVWD	300
Qy	248	-----	247
Db	301	VSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN	360
Qy	248	-----	292
Db	361	KALPAIEKTIKAKGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG	420
Qy	293	QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFPSCVMHEALHNHYTQKSLSLSP	352
Db	421	QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFPSCVMHEALHNHYTQKSLSLSP	480
Qy	353	GK 354	
Db	481	GK 482	

Search completed: March 23, 2005, 18:30:44
Job time : 144.475 secs

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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:07:03 ; Search time 94.5455 Seconds
(without alignments)
981.776 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMILLWVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	240	5	Aae27927 Human CC4
2	1243	100.0	240	6	Abb82836 Antibody
3	1166	93.8	240	2	Aay50156 Chimeric
4	1136	91.4	240	2	Aay50161 Human res
5	1125	90.5	240	4	Aau00815 Human Imm
6	1122	90.3	240	8	Adj65029 Plasmid P
7	1120.5	90.1	241	2	Aar28809 Vector pM
8	1090	87.7	244	3	Aay96305 Human IGF
9	1082	87.0	220	8	Adk52314 Human ant
10	1072.5	86.3	238	8	Adl23055 Humanised
11	1072.5	86.3	238	8	AdS88804 Humanised
12	1070	85.1	220	2	Aay50172 Antibody
13	1064	85.6	220	2	Aaw07528 Anti-HGF
14	1064	85.6	220	8	Adk52386 Human ant
15	1063	85.5	220	8	Adk52334 Human ant
16	1059	85.2	220	8	Adk52362 Human ant
17	1054	84.8	220	8	Adk52298 Human ant
18	1048	84.3	220	2	Aay08601 JPl112785
19	1044	84.0	242	4	Aau80338 Human mli
20	1044	84.0	242	4	Aau97949 HMG1 Fab
21	1044	84.0	242	4	Aau80039 HMG1 Fab
22	1040	83.7	238	6	Ada47330 TRX1 high
23	1040	83.7	238	6	Ada47332 TRX1 high
24	1040	83.7	238	8	Adp88450 Antibody
25	1040	83.7	238	8	Adp88426 Antibody

26	1040	83.7	238	8	ADQ87976	Adq87976 Light cha
27	1040	83.7	238	8	ADQ87964	Adq87964 Light cha
28	1034.5	83.2	238	8	ADL23052	Adl23052 Mouse/hum
29	1034.5	83.2	238	8	ADS88793	Ada88793 A mouse/h
30	1030	82.9	238	6	ADA47339	Ada47339 TRX1 high
31	1030	82.9	238	6	ADA47338	Ada47338 TRX1 high
32	1030	82.9	238	8	ADP88434	Adp88434 Antibody
33	1030	82.9	238	8	ADP88442	Adp88442 Antibody
34	1030	82.9	238	8	ADQ87972	Adq87972 Light cha
35	1030	82.9	238	8	ADQ87968	Adq87968 Light cha
36	1019.5	82.0	239	3	AAB03697	Aab03697 Immunoglo
37	1019.5	82.0	239	7	ADB72862	Adb72862 Human AAA
38	1014.5	81.6	238	5	ABG70744	Abg70744 Mouse/hum
39	1004.5	80.8	238	7	ADe64203	AdE64203 LL2LC pro
40	1001	80.5	234	8	ADR72766	Adr72766 Human mon
41	998.5	80.3	237	2	AAW73873	Aaw73873 Human ant
42	997.5	80.2	235	6	ABP71366	Abp71366 Anti-OPGL
43	997	80.2	238	3	AAW90931	Aaw90931 Humanised
44	997	80.2	238	5	ABB74900	Abb74900 Humanised
45	996	80.1	234	3	AAy92239	Aay92239 Human bon

ALIGNMENTS

RESULT 1
AAE27927
ID AAE27927 standard; protein; 240 AA.
XX
AC AAE27927;
XX
XX

DT 27-DEC-2002 (first entry)
XX
DE Human CC49 antibody light chain protein.
XX

KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS Homo sapiens.
XX
PN WO200260955-A2.
XX
PD 08-AUG-2002.
XX
PF 29-JAN-2002; 2002WO-US002373.
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
XX
(IDEC-) IDEC PHARM CORP.
XX
Braslawsky GR, Hanna N, Chinn P;
XX
WPI; 2002-698547/75.
DR N-PSDB; AAD45756.
XX

Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.

Example 1; Fig 5A; 74pp; English.

The present invention relates to domain deleted CC49 or C2B8 antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2B8 construct where the CH2 domain has been deleted. Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-Hodgkin's lymphoma. Antibodies of the invention are also used to treat

CC neoplastic disorder, colon cancer and hematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human CC49 light chain protein. This
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 240 AA;

Query Match 100.0%; Score 1243; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 3.8e-67;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSQAQVLMILLWVSGTCGDIIVMSQSPDSIAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 DB 1 MDSQAQVLMILLWVSGTCGDIIVMSQSPDSIAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY 120
 DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY 120
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
 DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
 QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2

ABB82836
 ID ABB82836 standard; protein; 240 AA.
 AC ABB82836;
 XX
 XX 31-MAR-2003 (first entry)
 DE Antibody huCC49 light chain.
 XX
 XX CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
 KW neuroprotective; antipneumatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 XX Homo sapiens.
 XX
 XX WO200296948-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002374.
 XX
 XX 29-JAN-2001; 2001US-0264318P.
 FR 16-NOV-2001; 2001US-0331481P.
 PR 21-DEC-2001; 2001US-0341859P.
 XX
 XX (IDEC-) IDEC PHARM CORP.

XX
 XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
 XX
 XX WPI; 2003-140446/13.
 DR N-PSDB; ABZ24020.
 XX
 XX Novel dimeric antibody useful for treating immune disorder and neoplastic
 PT disorder, has several non-covalently associated monomeric subunits.
 PT
 XX Example 1; Fig 5A; 78pp; English.
 FS
 XX The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,

CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
 CC detailed description of the various uses of (I)). The present sequence
 CC represents the antibody huCC49 light chain
 XX
 XX Sequence 240 AA;

Query Match 100.0%; Score 1243; DB 6; Length 240;
 Best Local Similarity 100.0%; Pred. No. 3.8e-67;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSQAQVLMILLWVSGTCGDIIVMSQSPDSIAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 DB 1 MDSQAQVLMILLWVSGTCGDIIVMSQSPDSIAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY 120
 DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY 120
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
 DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
 QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3

AA550156
 ID AA550156 standard; protein; 240 AA.
 XX
 XX AA550156;
 XX
 XX 17-OCT-2003 (revised)
 DT 31-JAN-2000 (first entry)
 XX
 XX Chimeric mouse/human F19 antibody light chain.
 DE
 XX
 XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
 KW humanisation; complementarity determining region, CDR; CDR grafting;
 KW reactive stroma; fibroblast; epithelial cancer; diagnosis;
 KW immune response; framework sequence; constant region; variable region;
 KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
 KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
 KW skin inflammation; tumour; immunogenicity; chimeric; light chain.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX Location/Qualifiers
 PH Key
 FT Peptide
 FT /note= "Leader peptide"
 FT Protein
 FT /note= "Mature chimeric mouse/human F19 light chain"
 FT Region
 FT /note= "Mature mouse F19 light chain variable region"
 FT Region
 FT /note= "Complementarity determining region (CDR) 1"
 FT Region
 FT /note= "CDR 2"
 FT Region
 FT /note= "CDR 3"
 FT Region
 FT /note= "Human kappa light chain constant region"

CC cancers and metastatic cancers. It is also useful for the detection of
CC activated stromal fibroblasts in a healing wound, inflamed skin or a
CC tumour in a human patient. (Updated on 17-OCT-2003 to standardise OS
CC field)

	Query Match	91.4%;	Score 1136;	DB 2;	Length 240;
	Best Local Similarity	90.0%;	Pred. No. le-60;		
	Matches 216; Conservative	12;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	1	MDSQAQVLMLLLVSGTCGDIVMSQPDSLAVSLGERVTLCNCKSSOSLILYSGNQKNYLA	60		
		: :			
Db	1	MEPTDLLWILLVWPSSGSDIVMTQPSDLAVSLGERATINCKSSQSLLYSRQKNYLA	60		
		: :			
Qy	61	WYQKPGQSFKLLIYWASARESGVPDRFSGSGSTDTFTLTISSVQAEADVAYYCQYYSY	120		
		: :			
Db	61	WYQKPGQPPLKLIWFVASTRRESGVDPDRFSGSGFGTDTFTLTISSLQAEADVAYYCQYFSY	120		
		: ~:			
Qy	121	PLTFGAGTKLELKHTVAAPSVFIFPPSDEQLKSCTASVVCCLNNFYPREAKVQMVDNAL	180		
		: ~:			
Db	121	PLTFGGQTKVEIKKHTVAAPSVFIFPPSDEQLKSCTASVVCCLNNFYPREAKVQMVDNAL	180		
		: ~:			
Qy	181	QSGNSQSPSVTEQDSKDSTYSLSSTLTILSKADYEKHVYACAEVTHQGJSSPVTKSFNRGEC	240		
		: ~:			
Db	181	QSGNSQSPSVTEQDSKDSTYSLSSTLTISKADYEKHVYACAEVTHOGJSSPVTKSFNRGEC	240		

RESULT 5	
AAU00815	
ID	AAU00815 standard; protein; 240 AA.
XX	
XX	AAU00815;
XX	
XX	
DT	01-JUN-2001 (first entry)
XX	
DE	Human Immunoglobulin superfamily, IgSF, protein #1.
XX	
KW	Human; Immunoglobulin superfamily protein; IgSF; Immune response;
KW	Inflammatory response; cell-cell interaction; cell-surface recognition;
KW	neural disorder; immune system disorder; muscular disorder;
KW	reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW	cardiovascular disorder; renal disorder; proliferative disorder; cancer;
KW	common variable adhesion deficiency syndrome; AIDS; SCID;
KW	acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;
KW	Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;
KW	Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;
KW	atherosclerosis; stroke; diabetes mellitus; Addison's disease;
KW	urticaria; severe combined immunodeficiency; antibody.

Key	Location/Qualifiers
Region	52..58
FT	/label= Immunogenic_epitope
FT	63..70
FT	/label= Immunogenic_epitope
FT	79..90
FT	/label= Immunogenic_epitope
FT	118..126
FT	/label= Immunogenic_epitope
FT	146..154
FT	/label= Immunogenic_epitope
FT	160..240
Domain	/label= Immunoglobulin_like_domain
FT	183..199
FT	/label= Immunogenic_epitope
FT	209..215
FT	/label= Immunogenic_epitope
FT	233..240
FT	/label= Immunogenic_epitope

XX	15-MAR-2001.
PD	
XX	29-AUG-2000; 2000WO-US023662.
XX	
XX	03-SEP-1999; 99US-0152248P.
PR	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	(NIJ/) NI J.
PA	
XX	Young PE, Ruben SM, Shi Y;
PI	
XX	WPI: 2001-203084/20.
DR	N-PSDB; AAS00145.
DR	
XX	Isolated nucleic acid molecule encoding a human secreted protein is used
PT	in preventing, treating or ameliorating a medical condition.
PT	
XX	Claim 11: Page 237: 247bp; English.
XX	
PS	

The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a diverse family of proteins involved in cell-cell interactions, cell-surface recognition, intercellular communication and immune and inflammatory responses. Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of tissues. Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention. Polypeptides of the present invention can be used to treat or prevent diseases or conditions such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. Polynucleotides of the invention are also useful in treating the above disorders. Examples of the disorders include common variable adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS), anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease, liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease, Huntington's disease, dementia, arteriosclerosis, stroke, diabetes mellitus, Addison's disease, urticaria, severe combined immunodeficiency (SCID). Many more examples of diseases and disorders are given in the specification.

[illegible]

RESULT 6
ADJ65029
ID ADJ65029 standard; protein; 240 AA.
XX
XX ADJ65029;
XX
DT 06-MAY-2004 (first entry)

Db 7 AQLGLLLWLPARGDVIWTPQSPDLAVSLGERATINCKSSGSLLYSTNQKYLAWYQQ 66
 Qy 65 KPGQSPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTF 124
 Db 67 KPGQPPKLLIYWASTRESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY-RTF 125
 Qy 125 GAGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWQVDNALQSGN 184
 Db 126 GRGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWQVDNALQSGN 185
 Qy 185 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
 Db 186 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 8

AA996305
 ID AA996305 standard; protein; 244 AA.

AC AA996305;

DT 16-AUG-2000 (first entry)

DE Human IGFAM-17 immunoglobulin.

XX Human; immunoglobulin; IGFAM-17; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.
 XX Homo sapiens.

FT Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= signal_peptide
 FT Domain /label= IGFAM-17
 FT Domain 40..120
 FT Domain /label= Ig_domain
 FT Domain 157..226
 FT Domain /label= Ig_domain

PN WO200029583-A2.

PD 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

PR 19-NOV-1998; 98US-00195853.

PR 22-DEC-1998; 98US-0113638P.

PR 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 PI Lu DAM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27397.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 91-92; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein
 CC IGFAM-17. Its gene was isolated from a cDNA library of intestine tissue.
 CC It is expressed in reproductive, gastrointestinal, immune and
 CC haematopoietic and cardiovascular tissue, where cancer and inflammation
 CC are common. The gene, protein, its antibodies, agonists and antagonists
 CC are suitable for diagnosing and treating many diseases, including cancer,
 CC immune system disorders (such as inflammation, AIDS, allergies, anaemia,
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,

CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus and ulcerative colitis), complications of
 CC cancer, haemodialysis and extracorporeal circulation, trauma and
 CC haematopoietic cancer (such as leukaemia) and infections caused by
 CC bacteria, viruses, fungi or parasites
 XX Sequence 244 AA;

Query Match 87.7%; Score 1090; DB 3; Length 244;
 Best Local Similarity 85.9%; Pred. No. 5.8e-58;
 Matches 207; Conservative 14; Mismatches 16; Indels 4; Gaps 1;

Qy 4 QAQVLMILLWWS-----GTGCDIVMSQSPDLAVSLGERVTLNCKSSQSLIYSGNQKYL 59
 Db 4 QTQVFISLLWISVLTAGAYGDIWTPQSPDLAVSLGERATITCKSSQSVFYNKKNYL 63

Qy 60 AWYQKPGQSPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYS 119
 Db 64 VWYQKPGQSPKLLIYWASTRESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYS 123

Qy 120 YPLTFGAGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWQVDNA 179
 Db 124 TPYTFGQGTREIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWQVDNA 183

Qy 180 LQSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRG 239
 Db 184 LQSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRG 243

Qy 240 C 240

Db 244 C 244

RESULT 9

ADK52314
 ID ADK52314 standard; protein; 220 AA.

XX AC ADK52314;

XX 20-MAY-2004 (first entry)

DT Human anti-MCP-1 variable region light chain #5.

DE monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 XX Antirheumatic; Nephroretropic; Antiarteriosclerotic; Antipsoaritic;
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.

XX Homo sapiens.

OS WO2004016769-A2.

PN 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 PI Bhakta S;

XX WPI; 2004-203794/19.

XX N-PSDB; ADK52313.

XX New human monoclonal antibody that binds to monocyte chemo-attractant
 CC protein-1 and is immobilized on an insoluble matrix, useful for
 CC diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 CC rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 20; 154pp; English.

XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
CC

Query Match	87.0%;	Score 1082;	DB 8;	Length 220;
Best Local Similarity	93.6%;	Fred. No. 1.6e-57;		
Matches 206;	Conservative 6;	Mismatches 8;	Indels 0;	Gaps 0;
QY	21	DIWMSQPSDLSVLSGBERTVLNCKSSOSLYSGNKNYLAWYQKQSPKLLIYWASIR	80	
DB	1	DIWMTQSPDLSVLSGERATINCKSSOSVLIYSSNNKYLWYQKQFPQPKLLIYWASIR	60	
QY	81	ESGVPRFRFGSGSGCTDFTLLTSSVQAEADVAVYQCQYYSPYPLTFGACTKLELKRITVAAPS	140	
DB	61	ESGVPRFRFGSGSGCTDFTLLTSSLQAEADVAVYQCQYYSTPLTFGGGTKVEIKRITVAAPS	120	
QY	141	VFIFFPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQSKDSTYS	200	
DB	121	VFIFFPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQSKDSTYS	180	
QY	201	LSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRRGEC	240	
DB	181	LSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRRGEC	220	

glycoprotein (WAG), useful for preparing a composition for treating or preventing stroke or other neurodegenerative disorders e.g., Alzheimer's disease.

Example 4; Fig 5; 67pp; English.

The present invention relates to a new altered antibody or its functional fragment, which binds to and neutralizes myelin associated glycoprotein (WAG) and comprises a light chain variable domain (VL) comprising complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The antibody is useful for preparing a composition for treating or preventing stroke or other neurodegenerative disorders in a human, e.g., traumatic brain injury, Alzheimer's disease, dementias, peripheral neuropathy, Parkinson's disease, Huntington's disease and multiple sclerosis. The present sequence is a humanised anti-WAG antibody.

Query Match	86.3%;	Score 1072.5;	DB 8;	Length 238;
Best Local Similarity	88.5%;	Pred. No. 6.4e-57;		
Matches 207;	Conservative 10;	Mismatches 16;	Indels 1;	Gaps 1;
QY	7	VLMLLILWVSGTGDIVMSQPSDLSAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKP	66	
		::: : :	::: : :	
Db	6	IILFLVATATGVHSDIVMTQSPDLSAVSLGERATINCKSSHVLYSSNQKYLAWYQKP	65	
QY	67	GOSPCLLIYWASARESGLVDFRFGSGSGTDFTLTISVQAEADVAVVYCOQYVYSLPFGA	126	
		::: : :	::: : :	
Db	66	GQPPCLLIYWASPRESGLVDFRFGSGSGTDFTLTISLQAEADVAVVYCHOYLS-SLTFQG	124	
QY	127	GTKLEIKRTVAAPSVFIPPSDBQLSGTASVCLLNFPYPRAKQVQWKVDNALQSGNSQ	186	
		::: : :	::: : :	
Db	125	GTKLEIKRTVAAPSVFIPPSDBQLSGTASVCLLNFPYPRAKQVQWKVDNALQSGNSQ	184	
QY	187	ESVTEQDSKDSYLSSTLTLSKADYEKKHKVYACEVTHQGLSPVTKSFNRGEC	240	
Db	185	ESVTEQDSKDSYLSSTLTLSKADYEKKHKVYACEVTHQGLSPVTKSFNRGEC	238	


```
OS Homo sapiens.
XX WO2004016769-A2.
XX 26-FEB-2004.
XX 19-AUG-2003; 2003WO-US026232.
XX 19-AUG-2002; 2002US-0404802P.
XX (ABGE-) AGENIX INC.
XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
XX Bhakta S;
XX WPI; 2004-203794/19.
XX N-PSDB; ADK52333.
XX New human monoclonal antibody that binds to monocyte chemo-attractant
XX protein-1 and is immobilized on an insoluble matrix, useful for
XX diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
XX rheumatoid arthritis or psoriasis.
XX Claim 2; SEQ ID NO 40; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
XX to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
XX for the preparation of a medicament useful for treating neoplastic or
XX inflammatory conditions. The neoplastic disease is selected from breast
XX cancer, ovarian cancer, bladder cancer, lung cancer, colon cancer,
XX stomach cancer, endometrial cancer, kidney cancer, glioblastoma,
XX pancreatic cancer or prostate cancer. The inflammatory condition is
XX selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
XX psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
XX antibodies are also useful for diagnosing the above diseases. It is also
XX useful for the determining the level of MCP-1 and MCP-1 family members in
XX patient samples. The present sequence represents a human anti-MCP-1
XX variable region light chain sequence.
XX
XX Sequence 220 AA;
XX
Query Match      85.5%; Score 1063; DB 8; Length 220;
Best Local Similarity 91.8%; Pred. No. 2.2e-56;
Matches 202; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
Qy      21 DIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNKNYLAWYQKPGOSPRLIYWASAR 80
Db      1 DIVMTQSPDSLAVSLGERATINCKSSQSLVLYSSNNKNYLVWYQQRPGQPPKLLIYWASTR 60
Qy      81 ESGVPDRFSGSGGTDFLTITSSVQAEDVAVYQCQYYSYPLTFAGTKLEKKTVAAPS 140
Db      61 ESGVPDRFSGSGGTDFLTITSSVQAEDVAVYQCQYYSYPLTFAGTKLEKKTVAAPS 120
Qy      141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSTYS 200
Db      121 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSTYS 180
Qy      201 LSSLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 240
Db      181 LSSLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 220
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Search completed: March 23, 2005, 18:34:45
Job time : 96.5455 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:11:05 ; Search time 24.6465 Seconds
(without alignments)
726.911 Million cell updates/sec

Title: US-10-058-069-9

Perfect score: 1243

Sequence: 1 MDSQAQVLMILLWVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	93.8	240	4	US-09-301-593-28
2	1136	91.4	240	4	US-09-301-593-36
3	1121.5	90.2	239	4	US-09-627-896B-22
4	1120.5	90.1	241	2	US-07-916-098A-56
5	1070	86.1	220	4	US-09-301-593-17
6	1064	85.6	220	3	US-08-952-235-1
7	1064	85.6	220	4	US-09-669-971-1
8	1019.5	82.0	239	3	US-08-812-586-29
9	1019.5	82.0	239	4	US-09-535-832A-30
10	994.5	80.0	235	4	US-09-472-087-14
11	994.5	80.0	235	4	US-09-472-087-65
12	991.5	79.8	233	4	US-09-472-087-15
13	991.5	79.8	233	4	US-09-472-087-67
14	987	79.4	236	4	US-09-859-053-34
15	985	79.2	234	4	US-09-472-087-17
16	985	79.2	234	4	US-09-472-087-69
17	977	78.6	236	4	US-09-859-053-38
18	974.5	78.4	239	4	US-10-000-489-8
19	969	78.0	234	3	US-09-049-672A-6
20	967	77.8	236	4	US-09-859-053-30
21	955.5	76.9	239	3	US-08-487-550-6
22	955.5	76.9	239	4	US-09-526-098-6
23	955.5	76.9	239	4	US-09-383-916-6
24	955	76.8	214	4	US-09-472-087-71
25	953	76.7	234	4	US-09-740-002-24
26	949	76.3	236	1	US-08-157-101A-5
27	944.5	76.0	235	3	US-09-171-945-97

28	941.5	75.7	232	1	US-08-704-744-80
29	941.5	75.7	235	3	US-09-171-945-99
30	941	75.7	218	2	US-08-887-352B-13
31	941	75.7	218	3	US-08-466-151-9
32	941	75.7	218	3	US-09-109-207C-13
33	941	75.7	218	3	US-08-296-005-13
34	941	75.7	218	3	US-08-466-163B-9
35	941	75.7	218	4	US-09-920-171-13
36	941	75.7	218	4	US-08-802-096-9
37	941	75.7	218	4	US-09-802-077-9
38	941	75.7	218	4	US-09-716-028-13
39	941	75.7	218	4	US-10-113-996-13
40	941	75.7	218	5	PCT-US96-13152-2
41	940.5	75.7	235	3	US-09-171-945-52
42	940	75.6	233	2	US-07-934-373C-25
43	940	75.6	233	3	US-08-437-642B-25
44	940	75.6	233	4	US-08-146-206C-25
45	940	75.6	233	4	US-09-705-686-25

ALIGNMENTS

RESULT 1

US-09-301-593-28
; Sequence 28, Application US/09301593A
; Patent No. 6455877
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.189001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-28

Query Match 93.8%; Score 1166; DB 4; Length 240;

Best Local Similarity 93.3%; Pred. No. 3.3e-88;

Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MDSQAQVLMILLWVSGTCGDIVMSQSPDLSVLSGERVTLNCKSSQSLLYSGNOKNYLA	60
Db	1	MDSQAQVLMILLWVSGTCGDIVMSQSPSLSVSGEKVTMCKSSQSLLYSRNOKNYLA	60
Qy	61	WYQKPGQSPKLLIYWASARESGVDPFSGSGSGTDFTLTITSSVQAEDVAVYYCOQYYSY	120
Db	61	WFQKPGQSPKLLIWFASRESGVDPFTGSGFGTDFTLTITSSVQAEDVAVYYCOQYFSY	120
Qy	121	PLTFGAGTKLEKRTVAAPSFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNAL	180
Db	121	PLTFGAGTKLEKRTVAAPSFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNAL	180
Qy	181	QSGNSQSVTEODSKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC	240
Db	181	QSGNSQSVTEODSKDSTYLSSTLTLSKADYKHKYACVTHQGLSSPVTKSFNRGEC	240

RESULT 2

US-09-301-593-36

```

; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-03-301-593-36

Query Match 91.4%; Score 1136; DB 4; Length 240;
Best Local Similarity 90.0%; Pred. No. 9.6e-86;
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAIVSLGERVTINCKSSQSLLYSGNQKNYLA 60
Db 1 METDTLLWILLWVPGSGDIVMTQSPDSLAIVSLGERATINCKSSQSLLYSRNQKNYLA 60

Qy 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120
Db 61 WYQKPGQPKLLIYFASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120

Qy 121 PLTGAGTKLEKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNV 180
Db 121 PLTGAGTKLEKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNV 180

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3
US-09-627-896B-22
; Sequence 22, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ CHERYL
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627.896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.

; FEATURE:
; OTHER INFORMATION: 3D1 light chain
US-09-627-896B-22

Query Match 90.2%; Score 1121.5; DB 4; Length 239;
Best Local Similarity 90.4%; Pred. No. 1.5e-84;
Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAIVSLGERVTINCKSSQSLLYSGNQKNYLA 60
Db 1 MDSQAQVLMILLWVSGTCGDIWVLTQSPDSLAIVSLGERATISCKSSQSLNSTRRENYLA 60

Qy 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120
Db 61 WYQKPGQPKLLIYWASTRESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCSQSYNL 120

Qy 121 PLTGAGTKLEKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNV 180
Db 121 -YTFGGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKNV 179

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 240
Db 180 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916.098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid

```

TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match 90.1%; Score 1120.5; DB 2; Length 241;
Best Local Similarity 92.4%; Pred. No. 1.8e-84;
Matches 218; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy 5 AQLVLLLLVSGTCTDVMQSPDLSVSLGERVTLNCKSSQSLLYSGNKNVLAWYQ 64
Db 7 AQLGLLLVLPFGARDVTMTQSPDLSVSLGERATINCKSSGSLYSTNKNVLAWYQ 66

Qy 65 KPGQSPKLLIYWASARESGVDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPTF 124
Db 67 KPGQPPKLLIYWASTRESGVDRFSGSGGTDFTLTISLQAEADVAVVYCOQYYSY-RTF 125

Qy 125 GAGTKLEKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 184
Db 126 GRGTKLEIKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGN 185

Qy 185 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 186 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 5
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 86.1%; Score 1070; DB 4; Length 220;
Best Local Similarity 93.2%; Pred. No. 2.3e-80;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPTFTGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPTFTGAGTKLEKRTVAAPS 120

Qy 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 7
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof

RESULT 6
US-08-952-235-1
; Sequence 1, Application US/08952235
; Patent No. 6207152
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,235
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-952-235-1

Query Match 85.6%; Score 1064; DB 3; Length 220;
Best Local Similarity 90.9%; Pred. No. 7e-80;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNVLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPTFTGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPTFTGAGTKLEKRTVAAPS 120

Qy 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 7
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof

Db 4 QTVFISLLWISG-AGIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNNKYLAWYQ 62
Qy 64 KQPGSPKLLIYWASARESVPDRFSGSGGTDFLTITSSVOAEDVAVVYCOQYYSYPLT 123
Db 63 KQPGQAPRLIYDASSRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCOQYGSPLT 122
Qy 124 FGAGTKLEKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
Db 123 FGGGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 182
Qy 184 NSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db 183 NSQSVTEQDSKDSYSLSSLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238

RESULT 10
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match 80.0%; Score 994.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.8e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
Qy 61 WYQKPGSPKLLIYWASARESVPDRFSGSGGTDFLTITSSVOAEDVAVVYCOQYYSY 120
Db 56 WYQRPQAPRLIYAGSSRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCOQYGS 115
Qy 121 PLTFGAGTKLEKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 116 PWTGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 175
Qy 181 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 11
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match 80.0%; Score 994.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.8e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRASQSI-----SSSFLA 55
Qy 61 WYQKPGSPKLLIYWASARESVPDRFSGSGGTDFLTITSSVOAEDVAVVYCOQYYSY 120
Db 56 WYQRPQAPRLIYAGSSRATGIPDRFSGSGGTDFLTITSLRLEPEDFAVYCOQYGS 115
Qy 121 PLTFGAGTKLEKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
Db 116 PWTGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 175
Qy 181 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 12
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15

Query Match 79.8%; Score 991.5; DB 4; Length 233;
Best Local Similarity 79.2%; Pred. No. 6.7e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDITGTEIVLTQSPGTLSLSPGERATLSCRTSVS-----SSYLA 53
Qy 61 WYQKPGSPKLLIYWASARESVPDRFSGSGGTDFLTITSSVOAEDVAVVYCOQYYSY 120

Db 54 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 113
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 180
Db 114 PFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 173
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 13

US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-67

Query Match 79.8%; Score 991.5; DB 4; Length 233;
Best Local Similarity 79.2%; Pred. No. 6.7e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRATSSV-----SSYLA 53
QY 61 WYQKPGQSKLLIYWASARESGVDFRFSGSGGTDFLTISRLEPEDFAVYVCOQYYSY 120
Db 54 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 113
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 180
Db 114 PFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNAL 173
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 14

US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 79.4%; Score 987; DB 4; Length 236;
Best Local Similarity 78.8%; Pred. No. 1.6e-73;
Matches 190; Conservative 27; Mismatches 18; Indels 6; Gaps 2;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRATSSV-----SSYLA 55
QY 61 WYQKPGQSKLLIYWASARESGVDFRFSGSGGTDFLTISRLEPEDFAVYVCOQYYSY 120
Db 56 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGS 115
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNA 179
Db 116 PMSFGGQTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNA 175
QY 180 LOSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 239
Db 176 LOSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 235
QY 240 C 240
Db 236 C 236

RESULT 15

US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match 79.2%; Score 985; DB 4; Length 234;
Best Local Similarity 78.3%; Pred. No. 2.3e-73;
Matches 188; Conservative 25; Mismatches 21; Indels 6; Gaps 1;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSCRATSSV-----SSYLA 54
QY 61 WYQKPGQSKLLIYWASARESGVDFRFSGSGGTDFLTISRLEPEDFAVYVCOQYYSY 120
Db 55 WYQKPGQAPRLIYGVSSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 114

Qy	121	PLTFGAGTKLELKRVTAAAPSVFI	PPPSDEQLKSGTASV	VCLNNFY	PREAKVQWKVDNAL	180
Db	115	PFTFGPTKVDIKRVTAAAPSVFI	PPPSDEQLKSGTASV	VCLNNFY	PREAKVQWKVDNAL	174
Qy	181	QSGNSQESVTEQDSKDSSTYLS	SLSTLTLSKADYKHKVYACEV	THQGLSSP	VTKSFNRGEC	240
Db	175	QSGNSQESVTEQDSKDSSTYLS	SLSTLTLSKADYKHKVYACEV	THQGLSSP	VTKSFNRGEC	234

Search completed: March 23, 2005, 18:35:51
Job time : 25.6465 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:26:57 ; Search time 73.9394 Seconds
(without alignments)
1074.721 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMMLLLWSGTCG.....EVTHQGLSSPVTKSPNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	93.8	240	9	US-09-301-593-28
2	1166	93.8	240	14	US-10-159-006-28
3	1136	91.4	240	9	US-09-301-593-36
4	1136	91.4	240	14	US-10-159-006-36
5	1125	90.5	240	9	US-09-799-514-8
6	1122	90.3	240	16	US-10-630-406-8
7	1121.5	90.2	239	9	US-09-249-011A-22
8	1115	89.7	240	17	US-10-938-353-24
9	1082	87.0	220	17	US-10-644-277-20
10	1070	86.1	220	9	US-09-301-593-17
11	1070	86.1	220	14	US-10-159-006-17
12	1064	85.6	220	9	US-09-995-693-1
13	1064	85.6	220	14	US-10-232-408-1

14	1064	85.6	220	17	US-10-644-277-92	Sequence 92, Appl
15	1063	85.5	220	17	US-10-644-277-40	Sequence 40, Appl
16	1059	85.2	220	17	US-10-644-277-68	Sequence 68, Appl
17	1054	84.8	220	17	US-10-644-277-4	Sequence 4, Appl
18	1047	84.2	239	9	US-09-825-012-9	Sequence 9, Appl
19	1044	84.0	242	10	US-09-819-266-26	Sequence 26, Appl
20	1040	83.7	238	14	US-10-171-452A-38	Sequence 38, Appl
21	1040	83.7	238	14	US-10-171-452A-56	Sequence 56, Appl
22	1040	83.7	238	15	US-10-353-708-38	Sequence 38, Appl
23	1040	83.7	238	15	US-10-353-708-56	Sequence 56, Appl
24	1040	83.7	238	16	US-10-731-984-3	Sequence 3, Appl
25	1040	83.7	238	16	US-10-731-984-27	Sequence 27, Appl
26	1030	82.9	238	14	US-10-171-452A-44	Sequence 44, Appl
27	1030	82.9	238	14	US-10-171-452A-50	Sequence 50, Appl
28	1030	82.9	238	15	US-10-353-708-44	Sequence 44, Appl
29	1030	82.9	238	15	US-10-353-708-50	Sequence 50, Appl
30	1030	82.9	238	16	US-10-731-984-11	Sequence 11, Appl
31	1030	82.9	238	16	US-10-731-984-19	Sequence 19, Appl
32	1014.5	81.6	238	16	US-10-467-253-14	Sequence 14, Appl
33	1010.5	81.3	235	17	US-10-938-353-60	Sequence 60, Appl
34	1007	81.0	220	9	US-09-917-410-5	Sequence 5, Appl
35	1006.5	81.0	235	17	US-10-938-353-32	Sequence 32, Appl
36	1002.5	80.7	235	17	US-10-938-353-44	Sequence 44, Appl
37	997.5	80.2	235	15	US-10-180-648-4	Sequence 4, Appl
38	997	80.2	238	14	US-10-216-484-129	Sequence 129, App
39	997	80.2	238	14	US-10-384-933-129	Sequence 129, App
40	995.5	80.1	239	15	US-10-292-088-56	Sequence 56, Appl
41	994.5	80.0	235	14	US-10-153-382-7	Sequence 7, Appl
42	994.5	80.0	239	15	US-10-292-088-40	Sequence 40, Appl
43	994	80.0	218	15	US-10-449-566-102	Sequence 102, App
44	993.5	79.9	239	15	US-10-292-088-16	Sequence 16, Appl
45	993	79.9	238	14	US-10-216-484-127	Sequence 127, App

ALIGNMENTS

RESULT 1

US-09-301-593-28
; Sequence 28, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-593-28

Query Match 93.8%; Score 1166; DB 9; Length 240;
Best Local Similarity 93.3%; Pred. No. 1.3e-64;
Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 MDSQAQVLMMLLLWSGTCGDIIVMSQSPDSLSVSLGERVTNLCKSSQSLLYSGNQNYLA 60
Db 1 MDSQAQVLMMLPLVWSGTCGDIIVMSQSPSSLSVSGEKVTMSCKSSQSLLYSRNKNYLA 60
Qy 61 WYQKPGSPKLLIYWASRESGVDPFRSGSGTGDTFTLTISVQAEDVAVYCOQYYSY 120

Db 61 WFOQKPGSPKLLIFWASTRESGVDRFTGSGFGDFNLTISSVQAEADVYDCQYFSY 120
121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Db 121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Qy 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2

US-10-159-006-28

; Sequence 28, Application US/10159006

; Publication No. US20030143229A1

; GENERAL INFORMATION:

; APPLICANT: Park, John E.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890002

; CURRENT APPLICATION NUMBER: US/10/159,006

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 09/301,593

; PRIOR FILING DATE: 1999-04-29

; PRIOR APPLICATION NUMBER: EP 98107925.4

; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: US 60/086,049

; PRIOR FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-159-006-28

Query Match 93.8%; Score 1166; DB 14; Length 240;
Best Local Similarity 93.3%; Pred. No. 1.3e-64;
Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Qy 61 WYQKPGQSPKLLIYWASARESVPDRFSGSGGTDFTLTISSVQAEADVYDCQYFSY 120
Db 61 WFOQKPGSPKLLIFWASTRESGVDRFTGSGFGDFNLTISSVQAEADVYDCQYFSY 120
Qy 121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Db 121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Qy 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3

US-09-301-593-36

; Sequence 36, Application US/09301593A

; Publication No. US20020052480A1

; GENERAL INFORMATION:

; APPLICANT: Park, John E.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 91.4%; Score 1136; DB 9; Length 240;
Best Local Similarity 90.0%; Pred. No. 9.1e-63;
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
Qy 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METDTLLWLLWVPGSSGDIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLA 60
Qy 61 WYQKPGQSPKLLIYWASARESVPDRFSGSGGTDFTLTISSVQAEADVYDCQYFSY 120
Db 61 WYQKPGQSPKLLIFWASTRESGVDRFSGSGGTDFTLTISSVQAEADVYDCQYFSY 120
Qy 121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Db 121 PLTFGAGTKLELKRIVAAPSVFIPPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNAL 180
Qy 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4

US-10-159-006-36

; Sequence 36, Application US/10159006

; Publication No. US20030143229A1

; GENERAL INFORMATION:

; APPLICANT: Park, John E.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890002

; CURRENT APPLICATION NUMBER: US/10/159,006

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 09/301,593

; PRIOR FILING DATE: 1999-04-29

; PRIOR APPLICATION NUMBER: EP 98107925.4

; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: US 60/086,049

; PRIOR FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-159-006-36

Query Match 91.4%; Score 1136; DB 14; Length 240;
Best Local Similarity 90.0%; Pred. No. 9.1e-63;
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
Qy 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METDTLLWLLWVPGSSGDIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLA 60

Qy	61	WTQKFGQSPKLLIIWASARGSGVPDRFSGSGGTDTFTLTISSVQAEDVAAVYVYCOQYYS	120
		: : : : : :	
Db	61	WTQKFGQSPKLLIIWASTRESGVPDRFSGSGGTDTFTLTISSVQAEDVAAVYVYCOQYYS	120
		: : : : : :	
Qy	121	PIITFGAGTKLEUKRTVAAPSVFIIPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	180
		: : : : : :	
Db	121	PIITFGGKTVEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL	180
		: : : : : :	
Qy	181	QSGNSQESVTEQDSKDSTYSISSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	240
		: : : : : :	
Db	181	QSGNSQESVTEQDSKDSTYSISSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	240
		: : : : : :	

RESULTS

```

RESOL1 3
US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar
; FILE REFERENCE: PT015P1
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-8

```

		Query Match	90.5%; Score 1125; DB 9; Length 240;	
		Best Local Similarity	90.3%; Pred. No. 4.3e-62;	
		Matches 214; Conservative	10; Mismatches 13; Indels 0; Gaps 0;	
QY	4	QAQVLMLLLWVGSTGCDIIVMSQPDSLSVSGIRVTLNCKSSQSLSLVSGNKNYLAWYQ	63	
		: : : : : : : : : : : : : : : : : : : :		
DB	4	QTQVFISLLMWISGAYGDIIVTQSPDSLAVSLGERATINCKSSQTVLVSSDNKNYLAWYQ	63	
		: : : : : : : : : : : : : : : : : : : :		
QY	64	QKFGSQPKLLIIYNASARESGVPDRFSGSGSSTDFTLTITSSVQADVAVVYCQQYYSYPLT	123	
		: : : : : : : : : : : : : : : : : : : :		
DB	64	QKFGQPPKLLIYNASTRESGVDPDRFSGSGSSTDFTLTITSSLQADVAVVYCQQYSTPYS	123	
		: : : : : : : : : : : : : : : : : : : :		
QY	124	FGAGTKLELRKTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG	183	
		: : : : : : : : : : : : : : : : : : ~:		
DB	124	FGOGTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG	183	
		: : : : : : : : : : : : : : : : : : ~:		
QY	184	NSQESVTEQDSKOSTYSLSLSTLTLSKADYEKHKYACEVTHQGIGSSPVTKSFNRGEC	240	
		: : : : : : : : : : : : : : : : : : ~:		
DB	184	NSQESVTEQDSKOSTYSLSLSTLTLSKADYEKHKYACEVTHQGIGSSPVTKSFNRGEC	240	

RESULT 6

RESOLUT 8
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbata
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630.406

```

; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

```

[illegible]

RESULT.7

```

US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22

```

	Query Match	90.2%	Score 1121.5	DB 9	Length 239
	Best Local Similarity	90.4%	Pred. No. 7.1e-62		
	Matches 217	Conservative	11	Mismatches 11	Indels 1
	Gaps	1			
Qy	1	MDSQAQVLLMLLLVSGTCGDIWMSQSPDSLAVSLGRVTLNCKSSQSLLYSGNKNYLA	60		
Db	1	MDSQAQVLLMLLLVSGTCGDIWVTQPSLAVSLGRATISCKSSQSLLNSRRTRENYLA	60		
Qy	61	WYQKQPGSQPKLLIYWASRESGVPDRFSGSGCTDFTLTISVQAEDVAVYCCQYYSV	120		

Db 61 WYQKPGQPKLLIYWASTRESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNL 120
Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 121 -YTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 179
Qy 181 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 240
Db 180 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 239

RESULT 8
US-10-938-353-24
; Sequence 24, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PP4
; CURRENT APPLICATION NUMBER: US/10/938.353
; PRIOR FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-24

Query Match 89.7%; Score 1115; DB 17; Length 240;
Best Local Similarity 89.5%; Pred. No. 1.8e-61;
Matches 212; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 4 QAQVLMILLVWGTCGDIWVSQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYQ 63
Db 4 QTVFISLLMISGADIVMTQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYR 63
Qy 64 QKPGQPKLLIYWASTRESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLT 123
Db 64 QKPGQPKLLIYWASTRESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLT 123
Qy 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSG 183
Db 124 FGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSG 183
Qy 184 NSQSVTEQDSKDSYSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 240
Db 184 NSQSVTEQDSKDSYSLSSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 240

RESULT 9
US-10-644-277-20
; Sequence 20, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendsch, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/644,277

; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-20

Query Match 87.0%; Score 1082; DB 17; Length 220;
Best Local Similarity 93.6%; Pred. No. 1.8e-59;
Matches 206; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASAR 80
Db 1 DIVMSQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASIR 60
Qy 81 ESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLTFGAGTKLEKRTVAAPS 120
Qy 141 VFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYTS 200
Db 121 VFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYTS 180
Qy 201 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 240
Db 181 LSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNREGC 220

RESULT 10
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 86.1%; Score 1070; DB 9; Length 220;
Best Local Similarity 93.2%; Pred. No. 9.9e-59;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASAR 80
Db 1 DIVMSQSPDLSVLSGERVTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYFASIR 60
Qy 81 ESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGTDFTLTISLQAEDVAIVYQSQSYNPLTFGAGTKLEKRTVAAPS 120
Qy 141 VFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYTS 200

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Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180
Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 11
US-10-159-006-17
; Sequence 17, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-08-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-17

Query Match 86.1%; Score 1070; DB 14; Length 220;
Best Local Similarity 93.2%; Pred. No. 9.9e-59;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLTVSGEKVTWSCSSQSLLYSRNQKNYLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVAAPS 140
Db 61 ESGVPDRFTGSGFGTDFLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVAAPS 120

Qy 141 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 200
Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180

Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 12
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180
Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220
```

```
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-No. US20020136721A1-2001
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

Query Match 85.6%; Score 1064; DB 9; Length 220;
Best Local Similarity 90.9%; Pred. No. 2.3e-58;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLTVSGEKVTWSCSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGGTDFLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVAAPS 140
Db 61 ESGVPDRFTGSGGTDFLTITSSVQAEADVAVYVCOQYYSYPLTFGAGTKLELKRVAAPS 120

Qy 141 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 200
Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180

Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 13
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
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; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

Query Match      85.6%; Score 1064; DB 14; Length 220;
Best Local Similarity 90.9%; Pred. No. 2.3e-58;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWSYQKPGQSPKLLIYWASAR 80
Db 1 DIMSQSPSSLTVSIGKVTYVCKSSQSLLYTSQKNYLAWSYQKPGQSPKLLIYWASTR 60
Qy 81 ESGVDRFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
Qy 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
Db 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
Qy 201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 15
US-10-644-277-40
; Sequence 40, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-40

Query Match      85.5%; Score 1063; DB 17; Length 220;
Best Local Similarity 91.8%; Pred. No. 2.7e-58;
Matches 202; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWSYQKPGQSPKLLIYWASAR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLYSSNNKNYLVYQQRPGOPPKLLIYWASTR 60
Qy 81 ESGVDRFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
Qy 141 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
Db 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
Qy 201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Search completed: March 23, 2005, 18:40:02
Job time : 75.9394 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:12:06 ; Search time 22.2222 Seconds
(without alignments)
1039.141 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMILLVWSGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	78.4	240	2 S06084	Ig kappa chain pre
2	972	78.2	216	2 J02041	Ig kappa chain Am3
3	936.5	75.3	215	2 J02042	Ig kappa chain NIG
4	926.5	74.5	215	2 J02044	Ig kappa chain NIG
5	894.5	72.0	215	2 A23746	Ig kappa chain V-I
6	887.5	71.4	215	2 J02043	Ig kappa chain NIG
7	833	67.0	220	2 A31790	Ig kappa chain V r
8	800	64.4	214	2 S68212	Ig kappa chain (Ma
9	757.5	60.9	225	2 S37484	Ig kappa chain - m
10	737	59.3	234	2 S14237	Ig kappa chain pre
11	728.5	58.6	219	2 S38865	Ig kappa chain - m
12	727.5	58.5	219	2 S32028	Ig kappa chain - m
13	727.5	58.5	230	2 S33161	Ig kappa chain - s
14	725.5	58.4	217	2 S42772	Ig kappa chain - m
15	724.5	58.3	219	2 PC4203	Ig kappa chain (mo
16	724	58.2	218	2 S68241	Ig kappa chain V r
17	722	58.1	218	2 J05810	monoclonal antibod
18	718.5	57.8	219	2 S16112	Ig kappa chain V r
19	718	57.8	234	2 S01320	Ig kappa chain pre
20	700.5	56.4	235	2 S25058	Ig kappa chain - m
21	696.5	56.0	225	2 J00029	Ig kappa chain pre
22	675	54.3	210	2 A56169	Ig kappa chain V r
23	662	53.3	145	2 P00014	Ig kappa chain pre
24	633	50.9	178	2 PT0219	Ig kappa chain V-C
25	619	49.8	138	2 S26040	Ig kappa chain pre
26	614	49.4	134	2 PC1214	Ig kappa chain pre
27	613.5	49.4	197	2 S29593	Ig kappa chain (WM
28	595	47.9	135	2 S2059	JC-kappa protein -
29	585.5	47.1	238	2 A49633	Ig lambda-like cha

30	577.5	46.5	229	2 A20969	Ig kappa chain pre
31	576	46.3	134	2 S49531	anti-Sm antibody V
32	573.5	46.1	133	2 P50023	Ig kappa chain pre
33	566	45.5	134	1 K4HU17	Ig kappa chain pre
34	565.5	45.5	133	1 K4HUJ1	Ig kappa chain pre
35	559	45.0	129	2 S40347	Ig kappa chain - h
36	554	44.6	135	2 S38807	Ig light chain V-J
37	549.5	44.2	138	2 A53261	Ig kappa chain pre
38	549	44.2	132	2 S46373	Ig kappa chain V-J
39	548	44.1	106	1 K3HU	Ig kappa chain C r
40	542	43.6	124	2 S40364	Ig kappa chain - h
41	540	43.4	113	2 A49260	antitumor monoclon
42	537	43.2	121	1 K4HU	Ig kappa chain pre
43	537	43.2	136	2 A49137	Ig kappa chain pre
44	533	42.9	120	2 G33932	Ig kappa chain pre
45	530.5	42.7	118	2 PT0356	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match	78.4%	Score	975	DB	2	Length	240
Best Local Similarity	76.2%	Pred. No.	1.6e-59				
Matches	183	Conservative	20	Mismatches	37	Indels	0
Qy	1	MDSQAQVLMILLVWSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQNYLA	60				
Db	1	MESQTQVLMILLVWSGTCGDFVMTQSPSSSLAVSAGETVTTINCKSSQSLFYSGNQNYLA	60				
Qy	61	WYQKPGQSPKLLIYWASARESGVDPDRPSGSGSGTDFLTITSSVQAEDVAVYCOQYYSY	120				
Db	61	WYQKPGQSPKLLIYWASTQSGVDPDRFIGSGSGTDFLTITSSVQAEDLAIYCLQYYET	120				
Qy	121	PLTGGAGTKLEKTVTAAPSFIIPPSDEQLKSGTASVVCILNNFYPREAKVQWVDNAL	180				
Db	121	PYTFGAGTKLEKTRADAPTIVSIFPPSTEQATGASVVCILNNFYPRDTSVKWKGDTGE	180				
Qy	181	QSGNSQSVTVQDQSKDSTYLSSTLTLSKADYKHVYACEVTHQGLSSPVTKSFNRGEC	240				
Db	181	RDGVLDSVTQDQSKDSTYSSSTLSLSKADYESHNLTCVWHKTSSTSPVVKSFNRNEC	240				

RESULT 2

J02041
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: J02041
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, Y.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: J02041
A:Accession: J02041

A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 972; DB 2; Length 216;
Best Local Similarity 86.8%; Pred. No. 2.2e-59;
Matches 191; Conservative 11; Mismatches 14; Indels 4; Gaps 3;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
Db 1 DIVLTQSPDFLAVSLGERATLNCKSSQSLY--NSKNFLAWYQKPGQ--PKLLI-WANVR 56
Qy 81 ESGVPDRFSGSGGTDFTLTISQVAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 57 ESGVPDRFSGSGGTDFTLTISQVAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 116
Qy 141 VFIPPPDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 117 VFIPPPDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 176
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 177 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 3
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 936.5; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 5.8e-57;
Matches 180; Conservative 18; Mismatches 17; Indels 5; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
Db 1 EIVLTQSPGTLISLSPGERATLISCRASQSV-----SNLYLAQYQKPGQAPSLIYDASSR 55
Qy 81 ESGVPDRFSGSGGTDFTLTISQVAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 56 ATGIPDRFSGSGGTDFTLTISGLEPEDFAVYVYCOQYDRPPTWTFGQTKVEIKRTVAAPS 115
Qy 141 VFIPPPDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 116 VFIPPPDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 175
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243

A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 926.5; DB 2; Length 215;
Best Local Similarity 81.0%; Pred. No. 2.8e-56;
Matches 179; Conservative 22; Mismatches 13; Indels 7; Gaps 2;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
Db 1 EVLTQSPATLISLSPGERATLISCRASQSV-----HSNLAQYQKPGQAPRLIYRASTR 54
Qy 81 ESGVPDRFSGSGGTDFTLTISQVAEDVAVYVYCOQYYSY-PLTFGAGTKLEKRTVAAP 139
Db 55 ATGIPARFSGSGGTDFTLTISLQSEDFALYVYCOQYNTWPPPLTFGGGTVKVEIKRTVAAP 114
Qy 140 SVFIPPPDSQKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
Db 115 SVFIPPPDSQKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 174
Qy 200 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 175 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 5
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <L80>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 894.5; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 4.2e-54;
Matches 178; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
Db 1 EIVLTQSPATLISLSPGERATLISGASQSV-----SSNLAQYQKPGQAPRLIYDASSR 55
Qy 81 ESGVPDRFSGSGGTDFTLTISQVAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 56 ATGIPDRFSGSGGTDFTLTISLQSEDFALYVYCOQYNTWPPPLTFGGGTVKVEIKRTVAAPS 115
Qy 141 VFIPPPDSQKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 116 VFIPPPDSQKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 175
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db 176 LSSSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 214

RESULT 6
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      71.4%; Score 887.5; DB 2; Length 215;
Best Local Similarity 79.2%; Pred. No. 1.3e-53;
Matches 175; Conservative 20; Mismatches 19; Indels 7; Gaps 2;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKVLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVMTQSPATLSVSGERATISCRASQSVATN-----VVWTKLQKQAPRLIIVDASTR 54

QY 81 ESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIK-RTVAAP 139
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 55 ATGVPAFSGSGSGTEFTLTISLSQSEDFAIYYCQHNAWPPFTGGTKVETKRRTVAAP 114

QY 140 SVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTY 199
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 SVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTY 174

QY 200 SLSSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 SLSSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 215
```

RESULT 7

Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Scura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

```
Query Match      67.0%; Score 833; DB 2; Length 220;
Best Local Similarity 70.9%; Pred. No. 6.6e-50;
Matches 156; Conservative 23; Mismatches 41; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKVLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNVLTWYQKPGQPKVLIYWASTR 60

QY 81 ESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRTVAAPS 140
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRADAAPT 120

QY 141 VFIPPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTDOODSKSTYS 180

QY 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 MSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220
```

RESULT 8

S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Tagaki, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

```
Query Match      64.4%; Score 800; DB 2; Length 214;
Best Local Similarity 70.1%; Pred. No. 1.1e-47;
Matches 150; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKVLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPSSLTAMSVGQKVTMSCKSSQSLNSRNQKNVLAWYQKPGQSPKLLVYFASTR 60

QY 81 ESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRTVAAPS 140
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRADAAPT 120

QY 141 VFIPPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTDOODSKSTYS 180

QY 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKS 234
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 MSSTLTLSKADYERKHVYACEVTHQGLSSPVTKS 214
```

RESULT 9

S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:G406254; PIDN:CAA49869.1; PID:G406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

```
Query Match      60.9%; Score 757.5; DB 2; Length 225;
Best Local Similarity 63.4%; Pred. No. 9.3e-45;
Matches 147; Conservative 32; Mismatches 46; Indels 7; Gaps 2;

QY 9 MLLLIWVSGTCGDIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKVLAWYQKPGQ 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VFLLLCVSGAGHSIVMTQPKLLLSAGDVTITCKASQV-----SNDVAVYQKPGQ 54

QY 69 SPKLLIYWASARESGVDPDRFGSGSGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGT 128
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 55 SPKLLIYASRYTGVDPDRFTGSGVGTDTFTTISTVQAEADVAVYCOQYYS-SYTFGGGT 113

QY 129 KLEIKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQES 188
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 KLEIKRADAAPTSGIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLN 173

QY 189 VTEQDSKSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 WTDQDSKSTYSMSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRNEC 225
```

RESULT 10

S14237

Ig kappa chain precursor (15C5) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S14237
R/Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A/Title: Construction and characterization of a recombinant murine monoclonal antibody
A/Reference number: S14236; MUID:91006173; PMID:2209622
A/Accession: S14237
A/Molecule type: mRNA
A/Residues: 1-234 <VAN>
A/Cross-references: EMBL:X56394; NID:g51622; PIDN:CAAJ9805.1; PID:g51623
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 737; DB 2; Length 234;
Best Local Similarity 58.8%; Pred. No. 2.4e-43;
Matches 141; Conservative 35; Mismatches 58; Indels 6; Gaps 1;

QY 1 MDSQAQVLMILLWVSGTCGDIVMSQPSDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
DB 1 MRPAPQLGILLWFPQIKDIDKMTQPSWYASLGERVTVTCRASODI-----NSYLS 54
QY 61 WYQKPGQSPKLIYIWASARESPGVDRFSGSGSGTDFTLTISVQAEDVAVYCOQYYS 120
DB 55 WIQKPGKSPKLIYRGNRLVAGVPSPFSGSGSGQDYSLTISSLEYEDVGVIYCLAYDEF 114
QY 121 PLTFGAGTKLELKRVTVAAPSVFIPPSDEQLKGGTASVCLLNFPYREAKVQWKVDNAL 180
DB 115 PFTFGSGTKLEIKRADAAPTVSIPTSPSEQLTSGGASVWFLNFPYKPDINVKWKIDGSE 174
QY 181 QSGNSQSVTEQDSKOSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 240
DB 175 RQGVLSNWTDDQDSKOSTYSMSLTLTQDEYRHNSTYCEATHTKSTSPVKSFRNEC 234

RESULT 11

S38865

Ig kappa chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C/Accession: S38865
R/Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A/Description: Combination of a defined specificity and desired isotype by cloning of an
A/Reference number: S38864
A/Accession: S38865
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-219 <KIP>
A/Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 58.6%; Score 728.5; DB 2; Length 219;
Best Local Similarity 63.2%; Pred. No. 8.5e-43;
Matches 139; Conservative 32; Mismatches 48; Indels 1; Gaps 1;

QY 21 DIVMSQPSDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLIYIWASAR 80
DB 1 ELVWTSPLSVSLGDAQSISCRSSQLVHT-NGNTYLHWYLOKPLSLIYIVSNR 59
QY 81 ESGVDRFSGSGSGTDFTLTISVQAEDVAVYCOQYYSYPLTFGAGTKLELKRVTVAAPS 140
DB 60 FSGVDRFSGSGSGTDFTLTISRVEADLGVYFCSQVTHVPWTFGGGTKLEIKRAAAPT 119
QY 141 VFTFPSPDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQSVTEQDSKOSTYS 200
DB 120 VSIPTSPSEQLTSGGASVWFLNFPYKPDINVKWKIDGSRQGVLSNWTDDQDSKOSTYS 179
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 240

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Db      180 MSSTLTLTKDEYRHNSYTCEATHKTSTSPIVKSPFNRGEC 219
          :|||:::||::|||::|||::|||::|||::|||::|||
RESULT 12
SS2028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkee, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      58.5%; Score 727.5; DB 2; Length 219;
Best Local Similarity 63.6%; Pred. No. 9.9e-43;
Matches 140; Conservative 29; Mismatches 50; Indels 1; Gaps 1;

Qy      21 DIVMSQPSDLAVSLGERVTLNCKSSQSLLYSNGKNYLAWYQKPQSPKLIIYWASAR 80
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 DVMTOSPLPVSIGDQASISCRSSQSIVHS-NGNTYLEWYQKPGQSPKLIIYKVSNR 59
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      81 ESGVPDRFGSGSGTDFTLTISSVOAEDVAHYCCQYYGYPLTFGGAGTKLELKRTVAAPS 140
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      60 FSGVPDRFGSGSGTDFTLKISRVEADLGVIYCFOGSHVPTFFGGTNLEIKRAADAAPT 119
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      141 VTIFPPSDQLKGSTASVVCLLNNFPYPRAKYQWKVDNALQGSNSQESVTEQDSKDSTYS 200
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      120 VSIFPPSSEQLTSGGASVCFVFNYPKDIINWKIKDGSRQGVLSNWTDDQSKDSTYS 179
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      201 LSSTLTLSKADYEKKHVACEVTHQGLSSPVTKSFNRGEC 240
          :|||::|||::|||::|||::|||::|||::|||::|||
Db      180 MSSTLTLTKDEYRHNSYTCEATHKTSTSPIVKSPFNRNEC 219

RESULT 13
SS3161
Ig kappa chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S33161
R;Toley, R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: S33161
A;Accession: S33161
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-230 <FOL>
A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>

Query Match      58.5%; Score 727.5; DB 2; Length 230;
Best Local Similarity 58.9%; Pred. No. 1e-42;
Matches 139; Conservative 40; Mismatches 50; Indels 7; Gaps 2;

Qy      6 QVLMLALL-VSCTCGDIVMSQPSDSLAVSLGERVTLNCKSSQSLLYSNGKNYLAWYQQ 64
         :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 QLGLGLLMLLPARGCDIQVTQSPSSLASLTERVITCRISQSV-----SNLYNWYQQ 54
         :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      65 KPQSQPKLIYWASARESGVPDRFGSGSGTDFTLTISSVOAEDVAHYCCQYYSYPLTF 124

```

Db 55 KPGQAPKLLIYYATRLHTDVPFRFSGSGGTDYTLTISNLEANDTATYVCQYESTPLAF 114
Qy 125 GAGTKLEKRTVAAPSVPFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
Db 115 GGGTNEIKRSDAQPVELFKPSEQLRTGTGVVVCVCLVNDFPYKDIINVKVKVDGVTQNSN 174
Qy 185 SQESVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 175 FQNSFTDQDSKDYSLSSSTLTLSSEYQSHNAYACEVSHKSLPTALVKSFNRKNEC 230

RESULT 14

S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 725.5; DB 2; Length 217;
Best Local Similarity 63.3%; Pred. No. 1.3e-42;
Matches 138; Conservative 31; Mismatches 48; Indels 1; Gaps 1;
Qy 23 VMSQSPDSLAVSLGRVTLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 82
Db 1 VMTQSPSLPVLGDAQISCRSSQSLVHT-NGNTYLHWYLPKPGQSPKLLIYKVSTRFS 59
Qy 83 GVPDRFSGSGGTDFTLTISSVQAEADVAVYYCQYYSPYPLTFGAGTKLEKRTVAAPSVP 142
Db 60 GVPDRFSGSGGTDFTFKISRVEADLGYYVCFQGSHPVPTFTGGGKLEIKRADAAAPT 119
Qy 143 IFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 202
Db 120 IFPPSDEQLTSGGASVVCFLNNFYPRKIDNVKWKIDGSRQNGVLSNWDQDSKDYSL 179
Qy 203 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 217

RESULT 15

PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein
C:Superfamily: immunoglobulin V region, immunoglobulin homology
F:1-112/Domain: V region #status predicted <CRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 58.3%; Score 724.5; DB 2; Length 219;
Best Local Similarity 62.7%; Pred. No. 1.6e-42;
Matches 138; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGRVTLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 80
Db 1 DVLMTQIPLSLPVSLGDAQISCRSSQSLVHT-NGNTYLEWYLPKPGQSPKLLIYKVSNR 59
Qy 81 ESGVDRFSGSGGTDFTLTISSVQAEADVAVYYCQYYSPYPLTFGAGTKLEKRTVAAPS 140
Db 60 FSGVDRFSGSGGTDFTLTKISRVEADLGYYVCFQGSHPVPTFTGGGKLEIKRADAAAPT 119
Qy 141 VFIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 200
Db 120 VSIFPPSDEQLTSGGASVVCFLNNFYPRKIDNVKWKIDGSRQNGVLSNWDQDSKDYSL 179
Qy 201 LSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 180 MSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

Search completed: March 23, 2005, 18:36:52
Job time : 23.2222 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:05:41 ; Search time 92.5253 Seconds
(without alignment)
1328.275 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMLLLVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	80.3	240	Q6PIH6	Q6pih6 homo sapien
2	985.5	79.3	235	Q6GMV9	Q6gmV9 homo sapien
3	983.5	79.1	239	Q8NEK0	Q8nek0 homo sapien
4	983	79.1	236	Q6PIL8	Q6pil8 homo sapien
5	977.5	78.6	235	Q6GMW0	Q6gmW0 homo sapien
6	977.5	78.6	235	Q6PJP2	Q6pjp2 homo sapien
7	976.5	78.6	239	Q8TCD0	Q8tcd0 homo sapien
8	975	78.4	236	Q6P5S8	Q6p5S8 homo sapien
9	974	78.4	236	Q6GMX8	Q6gmX8 homo sapien
10	968	77.9	234	Q72473	Q72473 homo sapien
11	965	77.6	236	Q6GMW1	Q6gmW1 homo sapien
12	965	77.6	236	Q6GMX0	Q6gmX0 homo sapien
13	963	77.5	236	Q723Y4	Q723Y4 homo sapien
14	959.5	77.2	239	Q6P491	Q6p491 homo sapien
15	958	77.1	236	Q6PIT5	Q6pit5 homo sapien
16	954	76.7	236	Q6PIH7	Q6pih7 homo sapien
17	953	76.7	236	Q6GMX9	Q6gmX9 homo sapien
18	935	75.2	236	Q6PIH4	Q6piH4 homo sapien
19	809	65.1	241	Q63ZX4	Q63zx4 mus musculus
20	767	61.7	238	Q66JS7	Q66jS7 mus musculus
21	742	59.7	236	Q7TS98	Q7ts98 mus musculus
22	725.5	58.4	219	Q65ZC0	Q65zc0 mus musculus
23	630	50.7	237	Q7S236	Q7s236 xenopus lae
24	617.5	49.7	243	Q6NTU5	Q6ntu5 xenopus lae
25	595	47.9	120	Q6P5R5	Q6p5R5 homo sapien
26	579	46.6	134	KV4C_HUMAN	P06314 homo sapien
27	565.5	45.5	133	KV4B_HUMAN	P06313 homo sapien
28	548	44.1	106	KAC_HUMAN	P01834 homo sapien
29	537	43.2	121	KV4D_HUMAN	P06312 homo sapien
30	532	42.8	114	KV4A_HUMAN	P01625 homo sapien
31	493	39.7	255	Q6KB05	Q6kb05 mus musculus

32	479	38.5	109	1	KV4D_HUMAN	P83593 homo sapien
33	470	37.8	236	2	Q8NEJ1	Q8nej1 homo sapien
34	464	37.3	236	2	Q6GMX4	Q6gmX4 homo sapien
35	460	37.0	236	2	Q6PIQ7	Q6piQ7 homo sapien
36	458	36.8	236	2	Q6IPO0	Q6ipQ0 homo sapien
37	456.5	36.7	235	2	Q6IN99	Q6in99 homo sapien
38	455.5	36.6	233	2	Q8TBC9	Q8tbc9 homo sapien
39	452.5	36.4	129	1	KV3L_HUMAN	P18135 homo sapien
40	449.5	36.2	129	1	KV3M_HUMAN	P18136 homo sapien
41	443	35.6	236	2	Q6GMX3	Q6gmX3 homo sapien
42	441.5	35.5	234	2	Q8N355	Q8n355 homo sapien
43	441.5	35.5	235	2	Q6PIK1	Q6piK1 homo sapien
44	440.5	35.4	234	2	Q6GMW3	Q6gmW3 homo sapien
45	439.5	35.4	235	2	Q99M11	Q99m11 mus musculus

ALIGNMENTS

RESULT 1

Q6PIH6 ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSRP; P01837; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.


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DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSP; P01834; 117Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 79.1%; Score 983.5; DB 2; Length 239;
Best Local Similarity 81.8%; Pred. No. 8.3e-74;
Matches 193; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 5 AQLVLLMLLVSGTCDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNQKNYLA 64
DB 5 AQLGLLMLVSGSGDIVMTQSPULPTVTPGEPASISCRSSQSLHSDGY-NYLDWYLQ 63

QY 65 KPGSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEADVAVYCYQYYSPLTF 124
DB 64 KPGSPQLLIYLSGNRASGVDPDRFSGSGSGTDFTLTKISKVEADVGIYVCHQGLQTPQTF 123

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 124 GQGIKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQSGN 183

QY 185 SOESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 184 SOESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073792; AAH73792.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.6e-73;
Matches 190; Conservative 26; Mismatches 18; Indels 7; Gaps 2;
QY 1 MDSQAVLMILLWVSGTCDIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNKNYIA 60
DB 1 MEAPQALLFLLLLPDTGTEIVMTQSPATLSVSPGERATLSCRASQSI-----SNNLA 54
QY 61 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 120
DB 55 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 114
QY 121 PLTFGAGTKLELRKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 179
DB 115 LLYFGQTKLELRKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 174
QY 180 LQSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGE 239
DB 175 LQSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGE 234
QY 240 C 240
DB 235 C 235
RESULT 6
Q6PJF2 ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Haleh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC016380; AAH16380.1; --
DR HSSP; P01937; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 77.9%; Pred. No. 2.6e-73;
Matches 187; Conservative 27; Mismatches 21; Indels 5; Gaps 1;
QY 1 MDSQAVLMILLWVSGTCDIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNKNYIA 60
DB 1 METPAQLFLLLLPDTGTEIVMTQSPATLSVSPGERATLSCRASQIV-----SSAYLA 55
QY 61 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 120
DB 56 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 115
QY 121 PLTFGAGTKLELRKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 180
DB 116 QGTGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA 175
QY 181 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 240
DB 176 QSGNSQESVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 235
RESULT 7
Q8TCD0 ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 78.6%; Score 976.5; DB 2; Length 239;
Best Local Similarity 80.2%; Pred. No. 3.2e-73;
Matches 190; Conservative 22; Mismatches 22; Indels 3; Gaps 2;

QY 5 AQLVLLLLVSGTCDIVMSQSPDLSAVSLGERVTLNCKSSQSLLYS-GNQKNVLAWQ 63
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 AQLGLLMLVPGSGGVMTQSPLSPLVTLTGQPASISCRSTQSLVYSDGN--TYLNNWFQ 62
QY 64 QKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTITSSVQAEDVAVVYCOQYYSPLT 123
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 QRPGQSPRLIYKVNRSQGVDPDRFSGSGSGTDFTLTKITRAEADVGIFYCQGTHTWEST 122
QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 183
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 FGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 182
QY 184 NSQSVTQDSKDSYISLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 NSQSVTQDSKDSYISLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCHI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 78.4%; Score 975; DB 2; Length 236;
Best Local Similarity 77.6%; Pred. No. 4.1e-73;
Matches 187; Conservative 29; Mismatches 19; Indels 6; Gaps 2;

QY 1 MDSQAQVLLVSGTCDIVMSQSPDLSAVSLGERVTLNCKSSQSLLYSGNQKNVLA 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 METPAQLFLLLVLPDTTGEIVLTQSGTSLSPFGERATILSCRATQVFSS-----HLA 55
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTITSSVQAEDVAVVYCOQYYSY 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 WYQRPQGAQPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITRLEPEFAVYFCQYGTGS 115
QY 121 P-LTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 PSLTFGGGTGTRVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 175
QY 180 LQSGNSQSVTEQDSKDSYISLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LQSGNSQSVTEQDSKDSYISLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 235

240 C 240
236 C 236
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منہ

Matches	187;	Conservative	19;	Mismatches	24;	Indels	6;	Gaps	1;
Qy	5	AQVLMILLWMVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKRYLAWYQQ	64						
Db	7	AQLGLGLLLWLRGARCDIQMTQSPSSLASVSGDRAVITTCRASQ-----NINNYLNWYQL	60						
Qy	65	KPGQSPKLLIYWASARESGVDPDRSGSGSGTDFTLTSSVQAQADVAVVYCOQYYSYPLTF	124						
Db	61	KPGKAPMLLIYAASSLQSGVPSRFGSGSGTDFTLTSSRPDPFATYVCOQSYNIPLTF	120						
Qy	125	GAGTKLELXRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN	184						
Db	121	GGGTINVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN	180						
Qy	185	SQSVTEQDSKDSITYLSLSTLTLSKADYEHKVVYACVTHQGLSSPYTKSFNRGEC	240						
Db	181	SQSVTEQDSKDSITYLSLSTLTLSKADYEHKVVYACVTHQGLSSPYTKSFNRGEC	236						

RESULT 13
Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723YA
AC Q723YA;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner S.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .

RESULT 14	
ID	Q6P491 PRELIMINARY; PRT; 239 AA.
AC	Q6P491;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DD	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OC	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skin;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP	SEQUENCE FROM N.A.
RC	TISSUE=Skin;
RA	Strausberg R.;
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC063599; AAH3599.1; -.
DR	HSSP; P01837; 1KCU.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig.v.
DR	Pfam; PF07654; Cl-set; 1.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; Igcl; 1.
DR	SMART; SM00406; Igv; 1.

DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
 Query Match 77.2%; Score 959.5; DB 2; Length 239;
 Best Local Similarity 78.8%; Pred. No. 8.2e-72;
 Matches 186; Conservative 22; Mismatches 27; Indels 1; Gaps 1;
 Qy 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLAWYQQ 64
 Db 5 AQLGLLLMLVPGSGDIVMTQTLSSPVTILGQPASISCRSSSLLHS-NGNTYLSMLHQ 63
 Qy 65 KPGSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCOOYYSYPLTF 124
 Db 64 RPOGPPRLIIYKISNRFSGVDPDRFSGSGAGTDFTLKISRVEADVGVYCYMCVSHFPRTF 123
 Qy 125 GAGTKLELKRITVAAPSVFIFFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 184
 Db 124 GQGTVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 183
 Qy 185 SOESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 240
 Db 184 SOESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 239

RESULT 15
 Q6PIT5
 ID TISSUE PRELIMINARY; PRT; 236 AA.
 AC Q6PIT5;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX Straubeberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029444; AAH29444.1;
 DR HSSP; P01607; 1AR2.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25741 MW; BD50AP071FE3E351 CRC64;
 Query Match 77.1%; Score 958; DB 2; Length 236;
 Best Local Similarity 79.7%; Pred. No. 1.1e-71;
 Matches 188; Conservative 16; Mismatches 26; Indels 6; Gaps 1;
 Qy 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNOKNYLAWYQQ 64
 Db 7 AQLGLLLMLVPGARCAIQLTQSPSSLSASVGERVTITCRASQGI-----SSALAWYQQ 60
 Qy 65 KPGSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCOOYYSYPLTF 124
 Db 61 KPGPPKLLIYDASTMESGVPSRFSGSGGTHFTLTITSSLQPEDFAFYCCQFKSYPRTF 120
 Qy 125 GAGTKLELKRITVAAPSVFIFFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 184
 Db 121 GQGTVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 180
 Qy 185 SOESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 240
 Db 181 SOESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 236

Search completed: March 23, 2005, 18:30:46
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